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GenCore version 5.1.6
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OM protein - protein search, using sw model

5, 2004, 10:55:48 ; Search time 60 Seconds May Run on:

(without alignments)
3569.517 Million cell updates/sec

4022 1 MAQRKNAKSSGNSSSSGSGS.....IVDVWHPELTPQQRRSLPAI 758 US-09-903-216-2 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

1586107 segs, 282547505 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

A_Geneseq_29Jan04:* Database :

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aab83919 A human a	Abg72365 Human asp	Human	Abu92053 Human pro	Aay33642 Human lab	Aau85544 Clone #48	Abu69516 Human lun	Abu66419 Lung canc	Abb61986 Drosophil	Aab73682 Human oxi	Aab43327 Human ORF	Abm68322 Photorhab	Aau29679 Novel hum		Aau28081 Novel hum	Aau31979 Novel hum	Abb60327 Drosophil	Aar70491 Leucocyto	Aab73672 Human oxi	Aar05804 C-termina	Aar98747 P. vivax	•		_	Abu23196 Protein e
ΠD	AAB83919	ABG72365	ADA00639	ABU92053	AAY33642	AAU85544	ABU69516	ABU66419	ABB61986	AAB73682	AAB43327	ABM68322	AAU29679	ABU21099	AAU28081	AAU31979	ABB60327	AAR70491	AAB73672	AAR05804	AAR98747	AAW97039	AAG66528	AAR97866	ABU23196
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% Query Match	100.0	100.0	100.0	33.7	33.2	32.8	32.8	32.8	23.2	6.8	6.8	6.5	6.9	5.4	5.4	5.3	5.1	5.1	9.9	4.9	4.9	4.9	4.9	4.9	4.9
Score	4022	4022	4022	1353.5	1334	1320	1320	1320	933	274.5	271.5	262	241	218.5	217.5	215	204.5	203.5	199	199	197.5	197.5	197.5	197.5	196.5
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Aay44506 Streptoco	Abu01047 S. pneumo	Aag46504 Arabidops	Abb68264 Drosophil	Aay96255 Kaposi's	Aay58500 HHV8 ORF	Aab62331 Amino aci	Abb05621 Kaposi's	Aaw03627 Human fol	Abul7264 Protein e	Ada36728 Acinetoba	Abu35669 Protein e		Abb67210 Drosophil	Abb59642 Drosophil	Aaw03626 Human thy	Ada56732 Human sec	Ada40577 Human sec	Abr47638 Human sec	Aay01148 Secreted	
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191.5	191.5	190.5	190.5	190.5	190.5	190.5	190.5	190	189.5	189.5	189.5	189.5	189	187.5	186.5	186	186	186	186	
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

AAB83919 standard; protein; 758 AA AAB83919; RESULT 1 AAB83919

23-JUL-2001 (first entry)

human aspartyl (asparaginyl) beta-hydroxylase (HAAH).

human aspartyl beta-hydroxylase; HAAH; malignant neoplasm; tumour. Epidermal growth factor-like domain; EGF-like domain; cancer;

Homo sapiens.

WO200135102-A2.

17-MAY-2001.

08-NOV-2000; 2000WO-US030738.

99US-00436184. 08-NOV-1999; (RHOD-) RHODE ISLAND HOSPITAL LIFESPAN PARTNER.

Carlson RI; De La Monte SM, Ince N, Wands JR,

WPI; 2001-329171/34.

N-PSDB; AAF89811.

Diagnosing malignant neoplasm in a mammal, involves contacting mammalian sample with antibody that binds to human aspartyl beta-hydroxylase polypeptide to form antigen-antibody complex and detecting the complex.

Disclosure; Page 5; 76pp; English.

The present sequence represents a human aspartyl (asparaginyl) beta-hydroxylase (HAAH) enzyme. Epidermal growth factor (EGF)-like domains of polypeptides are hydroxylated by HAAH enzymes. HAAH is used in the method of the invention. The specification describes a method for diagnosing a malignant neoplasm in a mammal. The method comprises contacting a body fluid with an antibody which binds to HAAH polypeptide under complex forming conditions, and detecting the antigen-antibody complex. The method is useful for diagnosing and prognosing a malignant neoplasm in a bodily fluid e.g. central nervous system (CNS)-derived body fluid, blood, serum, urine, saliva, sputum, lung effusion, and ascites fluid of mammal, where the neoplasm is derived from endodermal tissue and is selected from colon cancer, breast cancer, pancreatic cancer, liver cancer of

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bile ducts, and cancer of the CNS. HAAH antibodies, linked to a cytotoxic agent, are useful for killing tumour cells
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The invention relates to diagnosing a neoplasm and inhibiting tumour growth in a mammal, using an antibody that binds to human aspartyl (asparaginyl) beta-hydroxylase (HAAH). Diagnosing a neoplasm comprises contacting a tissue with a detectably-labelled antibody where an increase in level of antibody binding at tissue site compared to the level of binding to normal non-neoplastic tissue indicates the presence of a neoplasm at the tissue site. Inhibiting tumour growth in mammal involves administering the antibody conjugated as cyctoxic agent to a mammal. Also included are a method of conferring an immune response to a tumour cell in a mammal, by administering the antibody, a method of inducing an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAAH-specific immune response in a mammal, by administering to the mammal an HAAH polypeptide (or a polymucleotide composition encoding the polypeptide, or its degenerate variant), a fragment of HAAH comprising an extracellular domain and lacking a cytoplasmic domain of HAAH, an antibody or its fragment which binds to HAAH (where the antibody is FBSO, 86A, SC7 or 198), a hybridoma cell line chosen from hybridoma FBSO, HA386A, HA15CA and HA219B, and a fragment of HAAH which lacks enzymatic activity or alpha-ketoglutarate binding domain and epidermal growth
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/Jabel= Antibody binding_site
/note= "This region is specifically claimed in claim 36"
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/label= Antibody binding_site
/note= "This region is specifically claimed in claim 37"
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/note= "This region is specifically claimed in claim 38"
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/label= Catalytic_domain_1
/note= "This region is specifically claimed in claim 7"
immunostimulant; antibody; neoplasm; tumour; FB50; 86A; 5C7; 19B; brain tumour; glioma; gliona; glioblastoma; astrocytoma; haemangioma cancer; pancreatic carcinoma; colon cancer cancer; pancreatic cancer; liver cancer; cancer of the blie ducts; primary malignant CNS neoplasm;
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                                                                             metastatic CNS neoplasm.
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factor (EGF)-like domain. The methods are useful for diagnosing neoplasm in a mammal, inhibiting tumour growth in a mammal, conferring an immune response to a brain tumour cell (e.g. glioma, glioblastoma, astrocytoma or haemangioma) in a mammal, for conferring immune response to a pancreatic carcinoma cell and for inducing a HAAH-specific immune response in a mammal. The method is useful for diagnosing malignant neoplasms for mendodermal tissue, e.g. colon cancer, breast cancer, pancreatic cancer, liver cancer and cancer of the bile ducts. The method is also useful for diagnosing neoplasms of central nervous system (CNS) e.g. primary malignant CNS neoplasms of both neuronal and glial cell origin and metastatic CNS neoplasms, and for diagnosing brain present sequence represents human HAAH
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                                                                                                                                                                                                                                         100.0%; Score 4022; DB 6; 100.0%; Pred. No. 8.1e-311;
                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                               Sequence 758 AA;
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The present invention relates to a method for inhibiting tumour growth in a mammal. The method comprises administering to the mammal a compound, which inhibits the expression or enzymatic activity of a human aspartyl (asparaginyl) beta-hydroxylase (HAAH). The compound may inhibit HAAH hydroxylation of a NOTCH polypeptide. In particular, the compound may inhibit hydroxylation of an epidermal growth factor (EGF) like repeat sequence in a NOTCH polypeptide. The methods are useful for inhibiting tumour growth or killing tumour cells, or for diagnosing or prognosticating a malignant neoplasm. In particular, the tumour or neoplasm is colon cancer, breast cancer, pancreatic cancer, liver cancer, cancer of the bile ducts, or cancer or tumour of the central nervous system (CNS). The present sequence represents HAAH.
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                                                                                                                                                                                  HAAH hydroxylation; NOTCH polypeptide; epidermal growth factor-like repeat; EGF-like repeat; tumour cell; malignant neoplasm; colon cancer; breast cancer; pancreatic cancer; liver cancer; cancer of the bile duct; cancer the central nervous system;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting tumor growth or killing tumor cells (e.g. cancer of the colon, breast, pancreatic, liver or the central nervous system), by administering an inhibitor of the human aspartyl (asparaginyl) beta-
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                                                                                                                                                                      Tumour growth inhibition; human aspartyl (asparaginyl) beta-hydroxylase;
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                                                                                                                                Human aspartyl (asparaginyl) beta-hydroxylase (HAAH)
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                    ADA00639 standard; protein; 758
                                                                                                                                                                                                                                                                    cytostatic; enzyme; human.
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                                                                                            (first entry)
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(DMON/) DE LA MONTE S M.
(INCE/) INCE N.
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PEEAEPHTEPEEQVPVEAEPONIEDEAKEQIQSLLHEMVHAEHVEGEDLOQEDGPTGEPO 180
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                                                                                                                                                                                                                                                                         VNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVASLPDVPADLLK
                                                       QEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSODCNODMEEMMSEOENPDSSE
                                                                                                                                                                                                        FPVEEQQEVPPETNRKTDDPEQKAKVKKKKPKLLNKFDKTIKAELDAAEKLRKRGKIEEA
                                 QEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSE
                                                                                                   PVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSI
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2001US-0335703P.
2001US-0348887P.
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25-OCT-2001; 2
09-NOV-2001; 2
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The present invention relates to the isolation of human protein

modification and maintenance molecules (PMMM), and the polynucleotide

sequences encoding them. A total of 40 PMMM polypeptides (designated PMMM

-1 to PMMM-40) are disclosed. The sequences of the invention are useful

for diagnosing a condition or disease associated with the expression of

PMMM in a subject, preparing a polyclonal or monoclonal antibody, and

generating an expression profile of a sample containing the

polynucleotides. The diseases or conditions associated with decreased

expression or overexpression of PMMM are cell proliferation disorders

(e.g. cancer, atherosclerosis), neurological disorders (e.g. epilepsy,

Huntington's disease, stroke), immune/inflammatory disorders, (e.g. AIDS,

allergies), developmental disorders (e.g. hypothyroidism, Cushing's syndrome), gastrointestinal or epithelial disorders, and infections. The

PMMM polypeptides or their fragments are useful in screening compounds

con effectiveness as agonists or anteagonists of the polypeptide.

caltering the expression of the target polymcideide and compounds that

caltering the expression of the target polymcideide and compounds to specifically bind to, or modulate the activity of the polypeptide.

ABU92021-ABU92000 represent the human PMMM polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                 for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, atherosclerosis, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDGDFDVDDAKVLLGLKERSTSEPAVPPERAEPHTEPEEQVPVEAEPQNIEDEAKEQ1QS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                    Η,
                                                                                                                                                                                                                                                                                                                                            New human protein modification and maintenance molecules (PMMM), useful
                                                                                                                                                                                    Yue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----DSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 KETKHGGHKNGRKGGLSGTSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 GDGDFDVDDAKVLLGLKERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 RETKHGGHKNGRKGGLSGTSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDAD
                                                                                                                                       Lee SY;
                                                                                                                                                                               n PM, Kable AE, Tin P, Chien D;
Zheng W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 265;
                                                                                                                                       Yang J,
FA, Li J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1353.5; DB 6; Length
Pred. No. 4.2e-99;
2; Mismatches 0; Indels
                                                                                                                         Ramkumar J, Gorvag Ab, Lee EA, CLILL Tran UK, Becha SD, Duggan BM, Lee EA, Charlason PM, P. Sprague WW, Hafalia AJA, Chawla NK, Lehr-Mason PM, P. Varmis JP, Yao MG, Richardson TW, Tang TY, Jin P, Varmis JP, Yao MG, Richardson TW, Tang TY, Jin P, Varmis JP, Yao MG, Richardson TW, Tang TY, John Tree S, Blake JJ, Ho A, Zheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274 IEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPET 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 273-274; 311pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY33642 standard; protein; 255 AA.
28-NOV-2001; 2001US-0334145P.
06-DEC-2001; 2001US-0337451P.
14-DEC-2001; 2001US-0340584P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.7%;
92.5%;
                                                                                          (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259; Conservative
                                                                                                                                                                                                                                                                          WPI; 2003-430274/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                 N-PSDB; ACA92448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 VEET
                                                                                                                                                                                                                                                                                                                                                                                                               infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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AAY33642
ID AAY3
XX
AC AAY3
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241 SIFPVEEQQEVPPDT 255

RESULT 6

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This invention describes a novel polymucleotide and polypeptide sequence for the antigen detected by the antibody MCA 44-346. This antigen is designated Labyrinthin (Lab). Antibodies directed to the Labyrinthin (Lab). Protein are useful for the detection of Lab. The Lab protein is useful in diagnostic assays for cancer, e.g. to monitor the presence and amount of antibodies (this method is especially useful for cancer cells that have the Lab marker). As the Lab gene is not tissue-specific, it will detect cancer regardlass of which organ it occurs in. Peptides derived from Lab are used in the preparation of vaccines to prevent human cancer and/or to treat humans with cancer. Antibody MCA 44-346 is able to differentiate antigen detected by this antibody has not been elucidated in the prior art. Determination of the polypeptide and polymucleotide sequence of this antigen would enhance its usefulness in cancer diagnosis, treatment and prevention. The present invention discloses the sequence of the antigen recognized by the MCA 44-346 antibody. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents the human lab protein described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel Labyrinthin polynucleotides and polypeptides used as a diagnostic marker for cancer and in anticancer vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 PQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVIALLGVWTSVAVVWPDLVDYBEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 VPPEEAAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 PQQEDDEFLMATDVDDRFBTLEPEVSHEBTEHSYHVBETVSQDCNQDMEEMMSEQENPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                           Labyrinthin; human; cancer; marker; antigen; detection; antibody; MCA 44-3A6; diagnostic; vaccine; treatment; adenocarcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.2%; Score 1334; DB 2; Length 255; 99.6%; Pred. No. 1.4e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Fig 2; 34pp; English.
                                                                                                                                                                                                                                                                      99WO-US005365.
                                                                                                                                                                                                                                                                                                           98US-00040485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIFPVEEQQEVPPET 313
                  (first entry)
                                                    Human labyrinthin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254; Conservative
                                                                                                                                                                                                                                                                                                                                               (RADO/) RADOSEVICH J A.
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-580307/49.
N-PSDB; AAZ23609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 255 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Radosevich JA;
                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                          WO9947683-A1
                                                                                                                                                                                                                                                                    11-MAR-1999;
                                                                                                                                                                                                                                                                                                         17-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299
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Dp
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The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynucleotide and/or polypeptide is useful for treating a lung cancer in a patient. The polymorleotide is useful for treating a lung cancer in a patient. The polymorleotide is also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This is the amino acid sequence of a lung tumour associated protein. This jactent did not form part of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VPPEEAEPHTEPBEQVFVEAEPQNIEDEAKEQIQSLIHEMVHAEHVEGEDLQQEDGPTGE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mcnabb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 MVIALLGVWTSVAVVWFDLVDYBEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                     Lung tumour; cancer; T cell; immune response stimulator; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotide encoding a lung tumor polypeptide useful for stimulating and/or expanding T cells specific for a tumor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS,
Wang A, Fanger N, Switzer A, Moneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1320; DB 5; Length 25
Pred. No. 1.9e-96;
1; Mismatches 2; Indel8
                                                                                                                Clone #48005 (L979P) of lung tumour protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; SEQ ID NO 1806; 223pp; English.
                AAU85544 standard; protein; 255 AA
                                                                                                                                                                                                                                                                                                                                                                           2000US-00671325.
2000US-00677419.
2000US-00702705.
2000US-00736457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.8%;
                                                                                                                                                                                                                                                                                         10-JUL-2001; 2001WO-US022058.
                                                                                                                                                                                                                                                                                                                           2000US-00614124
                                                                                                                                                                                                                                                                                                                                                           2000US-00658824
                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-00849626
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jest Local Similarity 98.8
Matches 252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-164634/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABK39746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 255 AA;
                                                                                                                                                                                                                     WO200204514-A2.
                                                                                                                                                                                                                                                                                                                                                                           26-SEP-2000;
06-OCT-2000;
30-OCT-2000;
                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAY-2001;
                                                                                                                                                                                                                                                                                                                           11-JUL-2000;
                                                                                   21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                           08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                               13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                             29-AUG-2000;
                                                                                                                                                                                                                                                         17-JAN-2002
                                                 AAU85544;
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AAU85544
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The invention relates to a polymucleotide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences mentioned in the specification, or a sequence (S2) mentioned in specification, complement of S1, sequences consisting of at least 20 contiguous residues of S1, sequences that hybridise to S1, sequences having 75%, preferably 90%, identity to S1, or degenerate variants of S1. Also included are an isolated polypeptide (comprising a sequence (S3) selected from any one of the 4 amino acid sequences mentioned in the specification, a sequence cooded by the polymucleotide, or sequences having at least 70%, or preferably 90%, identity to a sequence encoded by the polymucleotide, or sequence encoded by the polymucleotide, or sequence cocded by the polymucleotide operably linked to an expression control sequence, a host cell transformed or transfected with the varies of a cancer specifically binds to the polypeptide, detecting the presence of a cancer in a patient, a fusion protein comprising the polypeptide, an oligonucleotide that hybridises to S1 under moderately stringent conditions, stimulating and/or expanding T cells specific for a tumour
                       298
                                                                                     Novel lung cancer polynucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer.
 PQQEDDEFLWATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS 238
                                                                                                                                                                                                                                                                                                                                                                            Human; lung cancer; lung tumour; cytostatic; vaccine; T cell expansion;
                                                                  SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang T, Switzer AP, Mcneill PD;
                                                                                                                                                                                                                                                                                                                                             Human lung cancer-associated protein L979P.
                                                                                                                                                                                                                                            ABU69516 standard; protein; 255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Page; 72pp; English.
                                                                                                                                   313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-MAY-2001; 2001US-00849626.
                                                                                                                                                              241 SIFPVEEQQEVPPDT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-DEC-2000; 2000US-00736457
                                                                                                                                                                                                                                                                                                             05-JUN-2003 (first entry)
                                                                                                                                 SIFPVEEQQEVPPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fanger GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWITZER A P. MCNEILL P D. CLAPPER J D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-352750/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BANGUR C S.
FANGER G R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ACA12072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WANG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2002197669-A1
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bangur CS,
                                                                  239
                                                                                                                                 299
                                                                                                                                                                                                                                                                             ABU69516;
                                                                                                                                                                                                                                                                                                                                                                                           CD4; CD8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CLAP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (/LIMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FANG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCNE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WANG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WANG/
                                                                                                                                                                                                               RESULT 7
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protein (comprising contacting T cells with the polymucleotide, protein or antigen-presenting cells, under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells) and inhibiting the development of a cancer in a patient (by incubating CD4 + and/or CD8 + T cells isolated from a patient with the polymucleotide, protein or antigen presenting cells that express the polymucleotide, protein or antigen proliferate, administering to the patient an effective amount of the proliferate, administering to the patient an effective amount of the proliferated T cells, and thus inhibiting the development of a cancer in composition for stimulating an immune response in a patient, and for treating a cancer in a patient (particularly lung cancer). The colymucleotide is useful for determining the presence of a cancer in a coligonucleotide is useful in pharmaceutical compositions, e.g. vaccines. The polymucleotide is also useful as a probe composition of rudcleic acid hybridisation, and in the design and proteins in tumour cells. An amplified portion of tumour polymentectide is useful for isolating a full-length gene from a suitable library. The present sequence is a protein encoded by a cDNA (full clibrary. The present sequence is a protein encoded by a cDNA (full clibrary. The present sequence is a protein encoded by a cDNA (full clibrary. The present sequence is a protein encoded by a cDNA (full clorm part of the printed specification, but was obtained in electronic form a tarter of the printed specification, but was obtained in electronic sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLIHEMVHAEHVEGEDLQQEDGFTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 PQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVERTVSQDCNQDMEEMMSEQENPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 SEPVVEDERLHHDTDDVTYQVYBEQAVYBPLENEGIEITEVTAPPEDNPVEDSQVIVEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTVPPEDNPVEDSQVIVEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lung cancer therapyand diagnosis associated protein #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lung cancer; cytostatic; vaccine; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1320; DB 6;
Pred. No. 1.9e-96;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU66419 standard; protein; 255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUL-2001; 2001US-00902941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.8%;
Best Local Similarity 98.8%;
Matches 252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIFPVEEQQEVPPET 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 SIFPVEEQQEVPPDT 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 255 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-NOV-2002.
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99US-00346492.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238
                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polypeptide associated with the compositions and methods for the therapy and diagnosis of lung cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                           composition for treating
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                                                                                                                                                                                                                                                                   Watanabe Y, Johnson JC, Retter MW;
anger GR, Vedvick TS, Bangur CS, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 12750.
                                                                                                                                                                                                                                                                                                                                      New polynucleotide, useful for preparing a composit
inhibiting development of cancer, e.g. lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1320; DB 6;
Pred. No. 1.9e-96;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                Example 5; SEQID NO 1807; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB61986 standard; protein; 422 AA.
                                                                                                                                                                                                                                                                                  Fanger GR,
        99US-00466867.
99US-00476300.
2000US-00519642.
2000US-00533077.
                                                               2000US-00546259.
2000US-00560406.
2000US-00589184.
                                                                                                                                                 26-SEP-2000; 2000US-00671325.
06-OCT-2000; 2000US-00677419.
30-OCT-2000; 2000US-00702705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.8%;
98.8%;
                                                                                                          2000US-00614124
                                                                                                                        2000US-00651563.
                                                                                                                                       2000US-00658824.
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                                                                                                                                                                                                                                                                   A, Wang T,
Carter D, F
                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 255 AA;
                                               22-MAR-2000;
10-APR-2000;
27-APR-2000;
20-JUN-2000;
11-JUL-2000;
29-AUG-2000;
09-SEP-2000;
                                                                                                                                                                                                                                                                     Henderson RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252;
                                                                                                                                                                                                                                                                                  Durham M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
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capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 PADLLKLSLKRRS--DRQQFLGHMRGSLLTLQRLVQLFPNDTSLKNDLGVGYLLIGDNDN 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 LEEFPESAGCKRGOVKFSVMQAKTHVWPHCGPTNCKLRAHLTLAAPEPEKASLRVAEQER 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 VASNQEFQTAGESCIENLRFLGHHRQATTIHELLINRLPEDPRLRNQLSLTYLMVNNLQQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 VEKVAVETLKLWPNNAVAQLHYGLALRQFHADYAKALPYLKYAVESGEEGTQEAFFYLSL 194
                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 GKIBEAVNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIBTYQEVASLPDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEKFPETTGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPK-EGCKIRCANETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 AKKVYEEVLSVTPNDGFAKVHYGFILKA-QNKIAESIPYLKEGIESGDPGTDDGRFYFHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDAMQRVGNK-EAYKWYELGHKRGHFASVWQRSLYNVNGLKAQPWWTPKETGYTELVKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent
Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           710 TWEEGKVLIFDDSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.2%; Score 933; DB 4; Length 42
45.0%; Pred. No. 2.5e-65;
tive 75; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                    Myers EW;
                                                                                                                                                                                                                                                                                    Li PWD,
                                                                                                                                                          23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                           23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 184; Conservative
                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                    Adams M,
                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75
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                  pharmaceutical
                                                                                     WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                           interactions
                                                                                                                                                                                                                                                                                    Venter JC,
                                                                                                                        27-SEP-2001
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590

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650 313 709

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Atterioscierosis; cirrhoses; cancer; endocrine disorder; diabetes mellitus; diabetes insipidus; dwarfism; hirsutism; amenorrhoea; diabetes insipidus; dwarfism; hirsutism; amenorrhoea; steeporosis; metabolic disorder; obesity; phenylkeronuria; hypercholesterolaemia; reproductive disorder; infertility; ovulatory defect; menstrual cycle defect; endometriosis; chromosome 22; polycystic ovary disease; spermatogenesis disruption; imporence; menological disorder; epileps; stroke, Alzheimer's disease; heurington's disease; Barkinson's disease; Creutfeldt-Jakob disease; Mennington's disease; mescular dystrophy; mood disorder; anxiety; schizophrenic disorder; infection; autoimmune disorder; anxiety; schizophrenic disorder; acquired immunodeficiency syndrome; AIDS; asthma; inflammatory disorder; acquired immunodeficiency syndrome; AIDS; asthma; allergy; Crohn's disease; acopic dermatitis; drug screening; transgenic animal; SNP detection; gene therapy; ss.
                                                                                                                             oxidoreductase protein; ORP; cell proliferative disorder;
                                                                                                     Human oxidoreductase protein ORP-15.
                          AAB73682 standard; protein; 369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE GENOMICS INC.
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-390245/41.
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                                                                                                                                                                                                                                                                                                                                                              WO200144448-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                           11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                       21-JUN-2001
                                                   AAB73682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yue H,
RESULT 10
              AAB73682
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07-DEC-2000; 2000WO-US033158.

99US-0172367P

Lal P, Tang YT, Hillman JL, Baughn MR, Azimzai Y,

Lu DAM;

Novel human oxidoreductase protein (ORP) useful for diagnosing, treating and preventing cell proliferative, neurological, viral, reproductive and autoimmune/inflammatory disorders associated with abnormal expression of

Claim 1; Page 110-111; 136pp; English.

Sequences AAB73668-AAB73694 represent 27 novel human oxidoreductase proteins, designated ORP-1 to ORP-27 respectively, and sequences AAB7223 represent CDNAs encoding ORP-1 to ORP-27. Human ORP proteins and nucleic acids are useful for diagnosing, treating or preventing cell proliferative disorders (e.g. arteriosclerosis, cirrhosis, psoriasis, cancers); endocrine disorders (e.g., type I or II diabetes mellitus, diabetes insipidus, dwarfism, hirsutism, amenorrhoea, osteoporosis); metabolic disorders (e.g., obesity, phenylketonuria, osteoporosis); metabolic disorders (e.g., obesity, phenylketonuria, ovulatory and menstrual cycle defects, endometriosis, polycystic ovary disorders (e.g., epilepsy, stroke, Alzheimer's disease, Huntington's disorders (e.g., epilepsy, stroke, Alzheimer's disease, Huntington's disease, parkinson's disease, meningitis, Creutzfeldt-Jakob disease, cerebral palsy, muscular dystrophy, mood, anxiety and schizophrenic disorders); viral, bacterial, fungal and parasitic infections; and autoimmune/inflammatory disorders such as acquired immunodeficiency syndrome (AIDS), allegajes, asthma, Crohn's disease, atopic dermatitis, counting multiple sclerosis, rheumatoid arthritis or ulcerative colitie. Human ORP proteins and nucleotides can be used to identify compounds which modulate their activity or expression. ORP nucleic acid sequences may also be used for assessing the toxicity of a test compound, to detect upstream sequences such as promoters and regulatory elements, and to create knock out or knock in animals or transgenic animals to model human

(CURA-) CURAGEN CORP.

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disease. Oligonucleotide primers derived from ORP gene sequences may be used to detect single nucleotide polymorphisms (SNPs) and for mapping the naturally occurring genomic sequences. Antibodise specific for ORP proteins may be used in the diagnosis of disorders associated with aberrant ORP expression, in assays to monitor patients being treated with ORP or modulators thereof, and for assessing toxicity of potential drugs
                                                                                                                                                                                                                                                                                                                                    125 KLYHNLQEYAKR----YSWSGMGRIHKGIREQGRYLNSRPSIQKPEVFFLPDLPTTPY 178
                                                                                                                                                                                                                                                                                                                                                                                                                          179 FSRDAQKHD--VEVLERNFQTILCEFETLYKAFSNCSLPQGWKMNSTPSGEWFTFYLVNQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      634 GRRNENACKGAPKTCTLLEKFPETTGCR-RGQIKYSIMHPGTHVWPHTGPTNCRLRMHLG 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 GVCVPRNCRKCPRTYRLLGSLRTCIGNNVFGNACISVLSPGTVITEHYGPTNIRIRCHLG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            693 LVIPKEGCKIRCANETRTWEEGKVLIFDDSFEHEVWQDASSF---RLIFIVDVWHPELTP 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 LKTP-NGCELVVGGEPQCWAEGRCLLFDDSFLHAAFHEGSAEDGPRVVFMVDLWHPNVAA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, open reading frame, ORFX, detection, cytostatic, hepatotropic, vulnerary, antipsoriatic, antiparkinsonian; nootropic, neuroprotective, anticorvulsant, osteopathic; antiarthritic; immunosuppressant, cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autocimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                          526 RFYFHLGDAMQRVGNKEAYKWYELG--HK----RGHF----ASVWQRSLYNVNGLKAQPW
                                                                                                                                                                                                                                                                                                                                                                                576 WTPKETGYTELVKSLERNWKLIRDEGLAVMDKAKGLFLPE--DENLREKGDWSQFTLWQQ
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                  6.8%; Score 274.5; DB 4; Length 369; 30.1%; Pred. No. 5.4e-13; tive 44; Mismatches 105; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ORFX ORF3091 polypeptide sequence SEQ ID NO:6182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB43327 standard; protein; 236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0127607P.
99US-0127636P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-1999; 99US-0127728P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000WO-US008621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                            75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 750 QORRSLPAI 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 AERQALDFI 364
                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                        Sequence 369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-1999;
02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB43327;
                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
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    8888888
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic, vulnerary; antiporvatic, antiparkinsonian; noctropic; neuroprotective; osteopathic; antiporvulsant; antiparkinsonian; noctropic; neuroprotective; osteopathic; cardiant; thrombolytic; coaquiant; vasotropic; antidabetic; hypotensive; cardiant; thrombolytic; cagulant; vasotropic; antidabetic; hypotensive; antiviral; antitheredian; antitheredian; antitheredian; cardiant; numinosuppressive; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative used to treat cancers, proliferative disorders, cardiovascular disease, disorders, osteoarthritis, graff vs host disease, cardiovascular disease, storage, systemic lupus erythematosus, severe combined immunodeficiency contracts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SCID), ALDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
                                                                                                                                                              Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                Claim 11; Page 5365; 5507pp; English
                       Leach M;
                                                                             WPI; 2000-602362/57.
                                                                                                           N-PSDB; AAC77536
                    Shimkets RA,
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Sequence 236 AA;

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                                                                                                                                                                                   651
                                                                                                                                                                                                                                                                                                  122 GSLRTCIGNNVFGNACISVLSPGTVITEHYGPTNIRIRCHLGLKTP-NGCELVVGGEPQC 180
                                                                                         544 YKWYELG--HK----RGHF----ASVWQRSLYNVNGLKAQPWWTPKETGYTELVKSLERN 593
                                                                                                                                                                                                                                                                          652 EKFPETTGCR-RGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETRT 710
                                                                                                                                        61
                                                                                                                                      4 YSWSGMGRIHKGIREQGRYLNSRPSIQKPEVFFLPDLPTTPYFSRDAQKHD--VEVLERN
                                                                                                                                                                                 594 WKLIRDEGLAVMDKAKGLFLPE--DENLREKGDWSQFTLWQQGRRNENACKGAPKTCTLL
                                                                                                                                                                                                                         62 PQTILCEFETLYKAFSNCSLPQGWKMNSTPSGEWFTFYLVNQGVCVPRNCRKCPRTYRLL
                                                 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                       711 WEEGKVLIFDDSFEHEVWQDASSF---RLIFIVDVWHPELTPQQRRSLPAI 758
6.8%; Score 271.5; DB 3; Length 236; 31.2%; Pred. No. 4.7e-13; tive 40; Mismatches 100; Indels 19
                                          72; Conservative
                       Similarity
Query Match
                       Local
                                            Matches
                                                                                                                                                                                 δ
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Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                     Photorhabdus luminescens protein sequence #1419.
                             ABM68322 standard; protein; 264 AA.
                                                                                       (first entry)
                                                                                                                                                                                                                             Photorhabdus luminescens
                                                                                                                                                                                                 whooping cough.
                                                                                        20-NOV-2003
                                                            ABM68322;
RESULT 12
                 ABM68322
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18-DEC-2001 (first entry)

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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of F. Luminescens and related species, to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. Luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. Luminescens and are able to alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        response or sensitivity to toxins and antibiotics produced by P. Imminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful the rapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           533 DAMQRVGNKEAYKWYELGHKRGHFASVWQRSLYNVNGLKAQPWW-TPKETGYTELVKSLE 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        552 EKFPETTGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETRTW 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 NNELRDWHCPLLEVHFSVLQPGTVIKPHCDLWNFTLNLHFAVDIPASHCEIIVANEARCW 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                                                                                                                                                                                   useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         592 RNWKLIRDEGLAVMDKAKGLFLPEDENLREKGDWSQFTLWQQGRRNENACKGAPKTCTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 NNADKIKQEINAVISGESQYITDYEHYLGTQKDWKALYLFKNGQPNNAVANILPATWHIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 DCLKRVED----MFYPLLQQR----APLQADAKYIMPGLSTTPWLDTNSFPQLQPLVTSLM
                                                                                                                                                                                                                                                                                                                                                                                            Genomic sequence of Photorhabdus luminescens and encoded polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                       Danchin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
&
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      712 EEGKVLIFDDSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 KEGECLLFDYSYQHEAYNRSDKHRICLLMDIWHPNLSFAEREALVLI 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
6.5%; Score 262; DB 6; Length 264;
Best Local Similarity 29.1%; Pred. No. 3.2e-12;
Matches 66; Conservative 39; Mismatches 114; Indels
                                                                                                                                                                                                                                                                    Taourit S, Glaser P, Frangeul L, Kunst F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; SEQ ID NO 1419; 1205pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU29679 standard; protein; 104 AA.
                                                                                                                                                                                                                    (CNRS ) CNRS CENT NAT RECH SCI
                                                                                            07-FEB-2002; 2002WO-IB003040.
                                                                                                                                            07-FEB-2001; 2001FR-00001659.
                                                                                                                                                                                             (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                            WPI; 2003-148459/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 264 AA;
WO200294867-A2
                                                                                                                                                                                                                                                                    Duchaud E, Ta
Buchrieser C;
                                              28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU29679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
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Nucleic acids encoding a range of human polypeptides, useful in genetic
                         Human, vaccination, gene therapy, nutritional supplement;
stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                         Claim 20; Page 179; 765pp; English.
        Novel human secreted protein #170
                                                                                                                                                                                                                       vaccination, testing and therapy,
                                                                                                                                                                             Liu C, Drmanac RT;
                                                                                                                16-APR-2001; 2001WO-US008656
                                                                                                                                 18-APR-2000; 2000US-00552929
                                                                                                                                         26-JAN-2001; 2001US-00770160
                                                                                                                                                                                             WPI; 2001-611725/70.
                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                             WO200179449-A2.
                                                             Homo sapiens.
                                                                                               25-OCT-2001
                                                                                                                                                                            ang YT,
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as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used

Sequence 104 AA;

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SSSSGSGSGSTSAGSSSPGARRETKHGGHKNGRKGGLSGTSFFTWFMVIALLGVWTSVAV 72
                                          0
6.0%; Score 241; DB 4; Length 104; 54.7%; Pred. No. 3.7e-11; iive 11; Mismatches 28; Indels
                                          Conservative
                    Similarity
                                    47;
  Query Match
                      Local
                                    Matches
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13 SAFIGICSSISVRAAAPPGIPORPSMDAHMIGRKGRLSXISFFIWSMVIALLGVWISVSV 72

엄 ð

73 VWFDLVDYEEVLGKLGIYDADGDGDF

73 VWFDLADYDDXLXALAIYDADGDVRF 98

ABU21099 standard; protein; 299 AA. 19-JUN-2003 (first entry) ABU21099 RESULT 14 ABU21099

Protein encoded by Prokaryotic essential gene #6626.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                      Zyskind JW;
Xu HH;
                                                                                                                      Ä,Ä
                                                                                                                      Ohlsen Forsyth
                                                                                                                      Haselbeck R,
Yamamoto R,
                                                                                                                                                                                              Claim 25; SEQ ID NO 49023; 1766pp; English.
                                                                                                                      Malone C,
Carr GJ,
                                                                     06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P
PEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                               21-MAR-2001; 2001US-00815242
                                                 21-MAR-2002; 2002WO-US009107
                                                                                                         (ELIT-) ELITRA PHARM INC.
      Burkholderia fungorum.
                                                                                                                       Zamudio C,
Trawick JD,
                                                                                                                                            WPI; 2003-029926/02
                                                                                                                                                    N-PSDB; ACA24969
                    WO200277183-A2.
                                   03-OCT-2002
                                                                                                                        Wang L,
Wall D,
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the nucleic acid inhibite proliferation of a cell. Also included are:

the 6213 antisense sequences given in the specification where expression

of the nucleic acid inhibite proliferation of a cell. Also included are:

concoding a polypeptide whose expression is inhibited by the antisense

concleic acid; (2) a host cell containing the vector; (3) an isolated

concleic acid; (2) a host cell containing the vector; (3) an isolated

contisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

contisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

contisention, (7) identifying a compound that influences the activity of

the gene product or that has an activity against a biological pathway

contiseration, (7) identifying a compound that influences the activity of

the gene product or that has an antibiotic cellular proliferation of an

conquired for proliferation-required gene or its gene product lies

con a gene on which the test compound that inhibits proliferation of an

corpanism acts; (9) manufacturing an antibiotic; (10) profiling a

compound's activity; (11) a culture comprising strains in which the gene

crompound's activity; (11) a culture comprising strains in which the gene

crompound's activity; (11) a culture comprising strains in which the gene

crompound's activity; (11) a culture comprising strains in which the gene

crompound's activity; (12) determining the extent

crompound's activity. The strains is present in a culture or collection of

strains; or (13) identifying the target of a compound that inhibits the

crompound activity; (10) and organism. The antisense mucleic acids are useful for

dentifying proteins or screening for homologous nucleic acids required

configured for proliferation to solate candidate molecules for rational K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent din on form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, The invention relates to an isolated nucleic acid comprising any one of

Sequence 299 AA;

9 551 HKRGHFASVWQRSL------YNVNGLKAQPWWTPKETGYTELVKSLERNWKL 596 5.4%; Score 218.5; DB 6; Length 299; 29.0%; Pred. No. 1.1e-08; Live 29; Mismatches 96; Indels 27. .1e-08; es 96; Conservative Local Similarity 62; Query Match Matches Best

597 IRDEGLAVMD----KAKGLFLPEDENLREKGDWSQFTLWQQGRRNENACKGAPKTCTLLE 652 ..

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553 KFPETTGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPK-EGCKIRCANETRTW 711
                                                                                                                           134 RIPSVKAAMFAQLP----PGGRLGLHRDPYAGALRYHLGLATPNHDGCAIVVDGETYSW 188
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IRDEAFALRDASHIRAATAYNDIGFNSFFRNGWRRFYLKWYGRPHPSAVALCPRTVELLG 133

EEGKVLIFDDSFEHEVWQDASSFRLIFIVDVWHP 745 : | : : | | : | | : | | 189 RDGEDIVFDETYLHYAFNDTQEDRIILFCDIERP 222

RESULT 15 AAU28081

AAU28081 standard; protein; 324 AA

AAU28081;

(first entry) 18-DEC-2001

Novel human secretory protein, Seq ID No 250.

ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen. Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;

Homo sapiens.

WO200166689-A2

13-SEP-2001

05-MAR-2001; 2001WO-US004942.

2000US-00574454. 2000US-00596193. 2000US-00616847. 2000US-00519705. 2000US-00665363 17-JUN-2000; 14-JUL-2000; 19-SEP-2000; 19-MAY-2000; 07-MAR-2000;

(HYSE-) HYSEO INC.

20-OCT-2000; 2000US-00693267

Zhou P; Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J; Tang YT, Zhao QA,

WPI; 2001-589934/66. N-PSDB; AAS44981

and treatment of Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment cancer, neurological, inflammatory, and autoimmune disorders.

Example 4; SEQ ID NO 250; 107pp; English.

and polymucleotides (II). (I) and (II) are useful for treating infilammentory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling (I), (II) and modularors of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, the polypeptide as well as for studying modulators of the polypeptides.
(I) induces the proliferation of neural cells and regeneration of nerve The invention relates to novel isolated human secreted polypeptides (1) Parkinson's disease, Huntington's disease, and amyotrophic lateral

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activity, regulation of haematopoiesis and is useful for treating myeloid activity, regulation of haematopoiesis and is useful for treating myeloid cor lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple solerosis, chaumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, used as such or or or circadian cycles of rhythms, creation, (I) affects biorhythms or circadian cycles of rhythms, creation, anabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitemins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28895 represent novel human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           625 WS-----QFTLWQQGR---RNENACKGAPKTCTLLEKFPETTGCRRGQIKYSIMHPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 WSPPLAPGCYQLLLYQAGRCQPSNCRRCPGAYRALRGLRSFMSAN--TFGNAGFSVLLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            674 THVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETRIWEEGKVLIFDDSFEHEVWQDAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 36.6%; Score 217.5; DB 4; Length 324; Similarity 36.6%; Pred. No. 1.5e-08; Conservative 19; Mismatches 56; Indels 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        733 --SFRLIFIVDVWHPELTPQQRRSL 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 EDGPRVVFIVDLWHPNVAGAERQAL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 324 AA;
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Local S...
53;
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Search completed: May 5, 2004, 11:02:20 Job time : 62 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                     Copyright
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OM protein - protein search, using sw model

5, 2004, 11:00:08 ; Search time 21 Seconds Run on:

(without alignments) 3472.056 Million cell updates/sec

US-09-903-216-2

758 4022 1 MAQRKNAKSSGNSSSSGSGS.....IVDVWHPELTPQQRRSLPAI Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	aspartyl beta-hydr	peptide-aspartate	cardiac junctate-1	O)	hypothetical prote	NF-180 - sea lampr	glutamate rich pro	hypothetical prote	zinc metalloprotei	cytadherence-acces	hypothetical prote	junctional sarcopl	hypothetical prote	Ë	flagellar antigen		aspartyl/asparagin	neurofilament trip	protein kinase - s	gene 11-1 protein	probable heat shoc	hypothetical prote			\sim	Ч	B2	hypothetical prote	
SUMMARIES	Ð	42	BABOH	JC7792	T18861	T47148	151116	A4555	HB3527	H95076	G64242	T42963	A45990	T08929	A33430	547436	S68191	A82601	A45669	849313	S00485	D96796	S52734	S46759	829796	S27776	T34518	483	S56271	T40168
	DB	7	-1	7	7	7	7	N	N	7	7	N	7	7	٦	N	7	N	7								7	7	۲3	7
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ф	Query	98.6	78.9	22.1	٩.	9.9	5.4	4.9	4.9	4.8	4.7	4.7	4.6	4.5	4.5	4.5	4.4	4.4	4.4	•	4.3	4.3	4.3	4.3	4.3	4.3	4.3		4.	4.2
	Score		3172	068	798	263.5	216.5	199	197.5	191.5	189.5	188.5	187	183	181	179.5	178.5	7	177	17		173.5	172.5	172	172	171.5	171	φ.		168.5
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neurofilament prot	probable membrane-	probable secreted	zinc metalloprotei	hypothetical prote	nucleolin - Africa	elastic titin - hu	hypothetical coile	translation initia	peptidylprolyl iso	hypothetical prote	hypothetical prote	myosin heavy chain	hypothetical prote	caldesmon - human	hypothetical prote
F52485	021	471623	E97944	25592	318874	I38346	T38077	F43483	S48647	271948	T21861	S21801	383081	JH0628	T46337
T52	AF102:	A7.	E3	H	0,			-	0,	_	٠.	٠,	щ	٠,	
2 T52	2 AF1	2 A71	2 E9	7 H	7	N	7	7	7	7	7		2 E	., H	7
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913 2	302 2 7	1192 2	1876 2	1624 2	651 2	7962 2	1957 2	1132 2	7	501 2	1877 2	1999 1 (299 2 1		4.0 992 2
913 2	302 2 7	4.2 1192 2	4.2 1876 2	4.1 1624 2	4.1 651 2	4.1 7962 2	4.1 1957 2	4.1 1132 2	411 2	4.1 501 2	4.1 1877 2	1999 1 (4.0 299 2 1		4.0

ALIGNMENTS

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C,Accession: 138423
R;Korioth, F.; Gieffers, C.; Frey, J.
Gene 150, 395-399, 1994
A,Title: Cloning and characterization of the human gene encoding aspartyl beta-hydroxylas
A,Reference number: 138423; MUD:95121937; PMID:7821814
A,Accession: 138423
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-757 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U03109; NID:g458031; PIDN:AAA82108.1; PID:g458032
C;Superfamily: peptide-agatate beta-dioxygenase; tetratricopeptide repeat homology
F;54-75/Domain: transmembrane #status predicted «TRM»
F;341-374/Domain: tetratricopeptide repeat homology <TTR»
                                              C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
aspartyl beta-hydroxylase - human
```

H 1; Gaps DB 2; Length 757; 98.6%; Score 3966.5; DB 2; Length 99.2%; Pred. No. 1e-195; tive 2; Mismatches 3; Indels Query Match Best Local Similarity 99.2 Matches 752; Conservative

120 61 IALLGVWTSVAVVWFDLVDYBEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPAVP 120 PEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQ 180 240 181 QEDDEFLMATDVDDRFETLEPBVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSE 240 300 300 360 121 PEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLIHEMVHAEHVEGEDLQQEDGPTGEPQ 180 FPVEEQQEVPPETNRKTDDPEQKAKVKKKKPKLLNKFDKTIKAELDAAEKLRKRGKIEBA 360 VNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVASLPDVPADLLK 420 421 LSLKRRSDRQOFLGHMRGSLLTLQRLVQLFPNDTSLKNDLGVGYLLIGDNDNAKKVYEEV 480 VNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVASLPDVPADLLK 420 9 9 61 IALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPAVP 1 MAQRICNAKSSGNSSSSGSGSGSTSAGSSSPGARRETKHGGHKNGRKGGLSGTSFFTWFMV QEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSODCNODMEEMMSEQENPDSSE 301 FPVEEQQEVPPETNRKTDDPEQKAKVKKKRPKLLNKFDKTIKAELDAAEKLRKRGKIEEA 1 MAQRICHAKSSGNSSSSGSGSGSTSAGSSSPGARRETIKHGGHKNGRKGGLSGTSFFTWFMV 241 PVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSI 361 121 181 241 301 à g 임 g DP g ð à ò δ a ò à d à

Qy 58 PMVIALLGVWTSVAVVWFDLVDXEEVLGKLGIXDADGDGDFDVDD 102	TSVÁVVWPDĽVDYBEVLAKAKDERXNLSEVLQGKĽGIYDADGDGDPD STSEPAVPPERAEPHTEPEGOVPVEAEPONIEDBAKEQIQSLIHEMV	Db 121 AKVLAGLKEKPAPKFTVPPEEADMYPWLEDQVLESPGRQNIFIEFT	Db 180PGENLPQEPEGPAEELQPDDHVFVGSDADDRYEPMGTGAVHEETEDSYHIEBTASPAY 237 Cy 223 NQDMEEMMSEQENVDSSEPVVEDERLHHDTDDVTYQVYEBQAVYEPLENEGIEITEVT 280	Db 238 SQDMEDMAYEQENPDSSERVVVDDAERTYQETDDVTYRDYDEQ 280	281DHAVDNSNTILEEPHMPPAEEQQEVPPETNKKADEPGKKGKVKKKFKLLNKFDKT	QY 341 IKAELDAAEKURKRGKIEEAVNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRG 400 	QY 401 AIETYQEVASLPDVPADILKLSIKRRSDRQOFLGHMRGSLLTLQRLVQLFRNDTSLKNDL 460	Qy 461 GVGYLLIGDNDNAKKVYEBVLSVTRNDGFAKVHYGFILKAQNKIAESIPYLKEGIESGDP 520	QY 521 GTDDGRFYFHLGDAMQRVGNKEAXKWYELGHKRGHFASVWQRSLYNVNGLKAQPWWTPKE 580	QY 581 TGYTELVKSLERNWKLIRDEGLAVMDKAKGIFLPEDENLREKGDWSQFTLWQQGRRNENA 640	Qy 641 CKGAPKTCTLLEKFPETTGCRRQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGC 700 Db 637 CKGAPKTCSLLDKFPETTGCRRQOIKYSIMHPGTHVWPHTGPTNCRLRWHLGLVIPKEGC 696	701 KIRCANETRIWEEGKVLIFDDSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI 758 	RESULT 3 JC7792 cardiac junctate-1 - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: Musculus (house mouse) C;Accession: JC7792 R;Hong, C.S.; Kwak, Y.G.; Ji, J.H.; Chae, S.W.; Kim, D.H. B;ochem: Biophys. Res. Commun. 289, 882-887, 2001 A;Tile: Molecular cloning and characterization of mouse cardiac junctate isoforms. A;Contents: Heart. A;Contents: Heart.	A,Molecule type: mRNA A,Residues: 1-270 cHON> A,Cross-references: 0B:AF702653 C;Comment: This protein, a Ca2+ binding protein. plays a role both in contractile and co C;Keywords: cardiac muscle, heart	Query Match 22.1%; Score 890; DB 2; Length 270; Best Local Similarity 63.9%; Pred. No. 8.8e-39; Matches 179; Conservative 30; Mismatches 57; Indels 14; Gaps 5; Qy 34 RETKHGGHKNGRKGGLSGTSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDAD 93
421	Qy 481 LSVTPNDGFAKVHYGFILKAQNKIAESIPYLKEGIESGDPGTDDGRFYFHLGDAMQRVGN 540	QY 541 KEAYKWYELGHKRCHFASVWQRSLYNVNGLKAQPWWTPKETGYTELVKSLERNWKLIRDE 600	OY 601 GLAVMDKARGLFLÞEDENIREKGDWSOFTLWQGRRNENACKGAPKTCTLLBKFPETTGC 660	OY 661 RRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKBGCKIRCANETRTWEBGKVLIFD 720 Db 660 RRGGIKYSIMHPGTHYWPHTGPTNCPLRMHLGLVIPKRGFKIRDANETRTWEBGKVLIFD 710	721 DSFEHEVWODASSFRIFTVDVWHPELTPOORRSLPAI 758	720	BABOH peptide-aspartate beta-dioxygenase (EC 1.14.11.16) - bovine NiAlternate names: aspartyl (asparaginyl) beta-hydroxylase	C;Date: 31-Dec-1993 Hasquence revision 10-Feb-1995 #text_change 11-Jun-1999 C;Accession: A42969; A39470; E39470; C29470; S27948 R;Jia, S.; VanDusen, W.J.; Diehl, R.E.; Kohl, N.E.; Dixon, R.A.; Elliston, K.O.; Stern,	U. Blol. Chem. 267, 14322-14327, 1992 J. Halle: cDNA cloning and expression of bovine aspartyl (asparaginyl) beta-hydroxylase. A.Reference number: A42969; MUID:92332646; PMID:1378441 A.Accession: A42969.	A;Nolectie type: mkNA A;Residues: 1-754 <jiaa> A;Cross-references: EMB:M91213; NID:g162693; PIDN:AAA03563.1; PID:g162694 A;Experimental source: brain</jiaa>	A.Note: sequence extracted from NCBI backbone (NCBIP:108534) R.Wang, Q.; VanDusen, W.J.; Petroski, C.J.; Garsky, V.M.; Stern, A.M.; Friedman, P.A. J. Biol. Chem. 266, 14004-14010, 1991 A.Title: Bovine liver aspartyl beta-hydroxylase. Purification and characterization.		A.Molecule type: protein A.Residues: 615, X., 617-630, XX., 633-634, XX., 639-641 <wa2> A.Accession: C39470 A.Molecule type: protein A.Residues: 311-347, X., 349, X., 351-373, X., 375-379, X., 381-382 <wa3> C.Comment: This enaryme uses ferrous iron as a cofactor, and while beta-hydroxylating the C.Comment: Appartic acid and asparagine residues in the EGF homology domain of certain p.C.Superfamily: peptide-aspartate beta-dioxygenase, tetratricopeptide repeat homology (XEW) words: 3lycoprotein; oxidoreductase, transmembrane protein C.Superfamily: peptide-aspartate beta-dioxygenase, tetratricopeptide repeat homology C.Steywords: 3lycoprotein; oxidoreductase; transmembrane protein F.2-56/Domain: theracellular #status predicted <irm> F.2-56/Domain: transmembrane #status predicted <irm> F.2-89-734/Ponduct: peptide-aspartate beta-dioxygenase, 56K form #status predicted <56K> F.3-78/Domain: transmembrane #status predicted <irm> F.2-89-734/Ponduct: peptide-aspartate beta-dioxygenase, 56K form #status predicted <56K> F.3-1-744/Ponduct: peptide-aspartate beta-dioxygenase, 56K form #status predicted <56K> F.3-1-744/Ponduct: peptide-aspartate beta-dioxygenase, 56K form #status predicted <56K> F.3-1-744/Ponduct: peptide-aspartates beta-dioxygenase, 56K form #status predicted <56K> F.3-1-744/F.3-1-74</irm></irm></irm></wa3></wa2>	F;337-370/Domain: tetratricopeptide repeat homology <tt1> F;371-404/Domain: tetratricopeptide repeat homology <tt2> F;13,96,466,702/Binding site: carbohydrate (Asn) (covalent) #status predicted Query Match 78.9%; Score 3172; DB 1; Length 754;</tt2></tt1>	Best Local Similarity 78.7%; Pred. No. 4.8e-155; Matches 612; Conservative 45; Mismatches 77; Indels 44; Gaps 6; QY 1 MAQRKWAKSSGNSSSSGSGSGSTSAGSSSPGARRETKHGGHKNGRKGGLSGTSFFTW 57

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587 VKSLERNWKLIRDEGLAVMDKAKGLFLPE--DENLREKGDWSQFTLWQQGRRNENACKGA 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            645 PKTCTLLEKFPETTGCR-RGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIR 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 PRIYRLLGSLRTCIGNNVFGNACISVLSPGTVITEHYGPTNIRIRCHLGLKTP-NGCELV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             583 YTELVKSLERNWKLIRDEGLAVMDKAKGLFLPEDENLREKGDWSQFTLWQQGRRNENACK 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     695 YSKFLKTVERQWATIRQEGMEVLKDCSDCWLDHNQQLVIDGQWKFFPIMSEQNFIKSSCE 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         643 GAPKTCTLLEKFPETTGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKI 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  755 RMPQTCLILQEFAASSNASKSDMHLSVLSSGASILPHCGPTNYHLQAHLGLVSPSE-ARI 813
                                              345 LDAAEKLRKRGKIEEAVNAFKELVRKYPOSPRARYGKAQCEDDLAEKRRSNEVLRGAIET 404
                                                                                                                                                                                                                      405 YQEVASLPDVPADLLKLSLKRRSDRQQFLGHMRGSLLTLQRLVQLFPNDTSLKNDLGVGY 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       575 VMMKRYEDARTVLKNVLANDPNHVIALAYYGYILKAHDDKVEOGVALMRKSLKNADNEIT 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 VEVLERNFOTILCEFETLYKAFSNCSLPQGWKMNSTPSGEWFTFYLVNÓGVCVPRNCRKC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        704 CANETRIWEEGKVLIFDDSFEHEVWQDASSF---RLIFIVDVWHPELTPQQRRSLPAI 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Petromyzon marinus (sea lamprey)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I51116
C;Accession: I51116
ExiJacobs, A.J.; Kamholz, J.; Selzer, M.E.
Brain Res. Mol. Brain Res. 29, 43-52, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Homo sapiens (man)
C.Jacession: Appr.2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C.Jacession: T47148
R.Blum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, March 2000
A.Reference number: 224379
A.Reference number: 247148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |::: || | : :| | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : | : | | : : | | : : | | : | : | | : : | | : | : | | : : | | : : | | : | : | | : : | | : : | | : | : | | : | : | | : | : | | : | : | | : : | | : : | | : : | | : : | | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                524 DGREYFHLGDAMQRVGNK-BAYKWYELGHKRGHFASVWQRSLYNVNGLKAQPWWTPKETG
                                                                                                  465 LLIGDNDNAKKVYBEVLSVTPNDGFAKVHYGFILKA-QNKIAESIPYLKEGIESGDPGTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 6.6%; Score 263.5; DB 2; 1 Similarity 35.4%; Pred. No. 6.5e-07; 63; Conservative 28; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein DKFZp761P039.1 - human (fragment)
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Best Local Similarity
Matches 63; Conserva
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A;Molecule type: mRNA
A;Residues: 1-186 <AAA>
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A;Introns: 18/1; 40/3; 74/1; 104/2; 139/1; 170/3; 385/3; 432/2; 464/3; 530/2; 609/3; 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:Z79596; NID:e1323798; PIDN:CAB01859.1; GSPDB:GN00028; CESP:K09A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable peptide-aspartate beta-dioxygenase (EC 1.14.11.16) - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 SDKVVEEKNDGDDEPHVSHREAQRLRRQHLRESRRDNRPRQGGNRECIHQDCPNRESLKP 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 IYDADGDGDFDVDDAKVLLGLKERSTSEPAVPPEEAEPHTEPEEQ-----VPVEAEPQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 NIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDG-----PTGEPQQEDDEFLMATDVDDR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 LDDDDDDDDDDDDDDDDDDDDDDDEKDDGNDAEKDDGDDDDDDDDDDBEDGKNKKTSVEAK 315
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                                                                                                                                            94 GDGDFDVDDAKVLLGLKERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDBAKEQIQS 153
                                                                                                                                                                                                                                65 GDGDFDVDDAKVLLGLKERSPSERTFPP-EAETHAELBEQAPEGADIQNVEDBVKEQIQS 123
                                                                                                                                                                                                                                                                                                                        LLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDFFLMATDVDDRFETLEPEVSHEETEHSYH 213
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A;Residues: 1-872 <WI2>
A;Cross-references: EMBL:Z79601; PIDN:CAB01887.1; GSPDB:GN00028; CESP:K09A9.6
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Query Match 19.8%; Score 798; DB 2; Length 872;
Best Local Similarity 26.8%; Pred. No. 2e-33;
Matches 191; Conservative 144; Mismatches 278; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 IEITEVTAPPEDNPVEDSOVIVEEVSIFPVEEQQEVPPET 313
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A,Accession: T23533
A,Status: preliminary; translated from GB/EMBL/DDBJ
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submitted to the EMBL Data Library, August 1996
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A;Residues: 1-872 <WIL>
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OY 225 DMERMASEQENPOSSEPUVEDERLHHDTDDV-TYQVYEEQAVYEPLENGGIEITEVT 280 175 NVSEVVEEKONGGESVEETPANEDSFEDVHTEQLDICHKTVDPEIVPWEIR 826 281 APPEDNYEEKONGGESVEETPANEDSFEDVHTEQLDICHKTVDPEIVPWEIR 8316 185 ::	REGULT 8 H893527 C. Date: 15-Sep-2000 #text_change 31-Dec-2000 C. Date: 15-Sep-2000 R. Strover, C. K.; Phan, X. O.; Erwin, A. L.; Mizoguchi, S. D.; Warrener, P.; Hickey, M.J.; Br. Adman, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A; Reference number: A20950; MUD: 20437337; PMLD: 10984043 A; Reference number: A20950; MUD: 20437337; PMLD: 10984043 A; Reference number: A20950; MUD: 20437337; PMLD: 109946838; PIDN: AAG04325.1; GSPDB: GN001. A; Residues: 1-312 & ASTON A; Residues: 1-312 & ASTON A; Residues: 1-312 & ASTON A; Generice: Strain PAO1 C; Generice: C; Generice: A; Generice: Strain PAO1 C; Generice: BAO936 Ouery Match Best Local Similarity 25-98; Pred. NO. 0.003; A; ERGREPASVWORSLINVORIKAOPWATEPRITEL
A,Title: The single lamprey neurofilament subunit (NF-180) lacks multiphosphorylation re A,Reference number: I51116; MUID:95287814, PMID:7770000 A,Scratus: preliminary: translated from GB/EMBL/DDBJ A,Molecule type: mRNA A;Molecule type: mRNA	RESULT 7 A45555 A45555 Glutamate rich protein - malaria parasite (Plasmodium falciparum) G)Species: plasmodium falciparum G)Species: plasmodium falciparum C)Species: plasmodium falciparum A)Title: primary structure and localization of a conserved immunogenic plasmodium falcip A)Title: primary structure and localization of a conserved immunogenic plasmodium falcip A)Title: primary structure and localization of a conserved immunogenic plasmodium falcip A)Title: primary structure and localization of a conserved immunogenic plasmodium falcip A)Total Species references: BMBL:M59706; MID:92131041; PMID:175153 A)Residues: 1-271 cBDR A)Residues: 1-271 c

702 IRCANETRIWEBGKVLIFDDSFEHEVWQDASSFRLIFIVDVWHP 745 185 IYVDGQPYAWRDGEDVWFDETFVHWVKNBTEQTRVILFCDIERP 228	Db 767 RESULT 10	-ITK
HB50NL 9 H955076 Zinc metalloproteinase ZmpB, probable [imported] - Streptococcus pneumoniae (strain TIGR C;Species: Streptococcus pneumoniae C;Species: O3-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 C;Accession: H95076 R;Tettelin, H: Nelson, K.E.; Paulsen, I.T.; Bisen, J.A.; Read, T.D.; Peterson, S.; Heid	4242 tadhe Speci Date: Acces Frase 7. Fuh	copj copj v-1s G642, c, d
S.L.; Lewis, M.R.; Radune, D.; Holtz .; Venter, J.C.; Dougherty, B.A.; Mo nt isolate of Streptococcus pneumoni ID:11463916	Science 270, A,Title: The A,Reference A,Reference A,Accession: A,Status: pre A,Molecule ty A,Residues: 1	397. min combe G64. lim lim
tus: preliminary ecule type: DNA didues: 1-1881 «KUR> ss-references: GB.AE005672; PIDN:AAK74809.1; PID:g14972138; GSPDB:GN00164; TIGR:SP4 erimental source: strain TIGR4 e: SP0664	A;Cross-refer A;Experimenta C;Genetics: A;Genetic cod Query Match Beet Local	ference tal sc code: S code: S
Query Match 4.8%; Score 191.5; DB 2; Length 1881; Best Local Similarity 21.6%; Pred. No. 0.06; Matches 138; Conservative 82; Mismatches 226; Indels 193; Gaps 30;	Marches	FDI
111 ERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGED 168 		
169 LQQEDGPTGEPQQEDDFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQ-DME 227 	Db 1151 Qy 166	GEI
EMMSEQENPDSSEPVVEDERIJHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPP ::		
BDBDSQVIVEEVSIPPVE	Db 1263 QY 270	YDE
EVPPETNRKTDDPEQKAKVKKKKPKLINKFDKTIKAELDAAEK	Db 1322 Qy 324	AK.
LRKRGKIEBAVNAFKELVRKYPQSPRARYGKAQ	Db 1379 Qy 384	CE PO
	М	
556 IKSITAELKKGEBVINTVVLTDDKVTTETISAAFRNLBYYKEYTLSTTMIYDRGNGEETE 615	Qy 442 Db 1418	H H
408 VASLPDVPADLLKLSLKRRSDRQQFLGHMRGSLLTLQRLVQLFPNDTSLKNDLGVGYL 465 ::		
LIGDNDNAKKVYEEVLSVTPNDGFAKVHYGFILK-AQNKIAES-IPYLKEGIES	DD 1463 QY 555	HE
666 KITSNNÖKTTELAVKNIEETTVNGTPVYKVTAIADNLVSRTADNKFEEEEVHYIEK 721 518 GDPGTDDGREYFHLGDAMORVGNKEAYKWYELGHKRGHFASVWORSLYNVNGLKAOPW 575	Db 1510	MO
		AK
576 WIPKETGYTELVKSLERNWKLIRDEGLAVMDKAKGLF 612	Db 1552	-

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Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
i Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.N.
J.C.
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:es: GB:U39723; GB:L43967; NID:g1046092; PID:g1046097; TIGR:MG386
:ource: strain G-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLKERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIOSLIHEMVHAEHVE 165
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                                                                                                                                                                                                                                                                                                                                                                                                essory protein (hmw1) homolog MG386 - Mycoplasma genitalium
lasma genitalium
995 #sequence_revision 17-Nov-1995 #text_change 07-Dec-1999
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hilarity 22.3%; Pred. No. 0.063;
Conservative 78; Mismatches 205; Indels 213; Gaps
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per: A64200; MUID:96026346; PMID:7569993
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-----KLLSSEGKQFAITELEHPLF 793
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49

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256 AAVSKQEQKDQYAFCRYMIDIFVHGDLKPGQSPAIPPPSPTEQAS---RPTPALPTPEEK 312
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                                                                                                                                                                                                                                                                                                                                                                                                 93 ------DGDGDFDVDDAKVLLG-LKERSTSEPAVPPEEAEPHTEPEEQVPV--- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 DDVTYQVYEEQAVY-----EPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQ 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 GFFSILSDIISSDGDEEDDEGDEDTAKGEIBEPPLKRKDIHKEKIEKOEKPERKIPTKVV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 ----EAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPIGEPQQEDDEFLMATDV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 HKEKEKEKEKVKEKEKPE----KKATHKEKLEKKEKPETKTVTYGEKKARTK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 ----EKIEEKTKKE-----BKGVKQEKVKQTVAKAKEVQKTPKPK-----BKESKET
                                                                                                                                                                                                                                                              --SSPGARRETKHGGHKNGRKGGLSG
                                                                                                                                                                                                                                                                                                                   9 NASTITIVIDSKNGSVPKSPGKVLKRIVIEDLVIIFSSPAA-------
                                                                                                                                                    4.6%; Score 187; DB 2; Length 706;
21.0%; Pred. No. 0.029;
tive 77; Mismatches 165; Indels 152;
                                                                                                                                                                                                                                                                                                                                                                        52 TSFFTWFMVIALLGVWTSVAVVWFDLVDXEEV----LGKLG-----IYDA-
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                                                                                                                                                                                                                                                                   6 NAKSSGNSSSSGSGSGSTSAGS----
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                                                                                                                                                         Query Match
Best Local Similarity 21.0%
Matches 105; Conservative
                   A, Molecule type: mRNA
A, Residues: 401-620 <PEN>
C, Superfamily: histone H1
                                                                                                    C; Keywords: glycoprotein
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A; Residues: 1-763 <BI
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A:Accession: S45704
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A;Note: sequence extracted from NCBI backbone (NCBIN:133603, NCBIP:133604)
A;Pong, M.; Fan, H.; Kirley, T.L.; Caswell, A.H.; Schwartz, A.
FEBS Lett. 348, 17-20, 1994
A;Title: Structural diversity of triadin in skeletal muscle and evidence of its existend
A;Reference number: S45704; MUID:94298946; PMID:8026576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 GIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPETNRKTDDPEQKAKVKKKKPK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GESKEDDEDDEÉEBDEÉDDEBEEDÉ-----BÉEDÉDEEDEEDEEDEÉBDEDEEDEEGDR 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 LLNKFDKTIKAELDAAE-----KLRKRGKIEEAVNAFKELVRKYPQSPRARYGKA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 GDGDFDVDDAKVLLGLKERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       556 EEEEEDEEDEEDEEDEEEKEDBEEKEDEEEKEDEEDEDEBEKEDDED-----EEE-----EEE 603
                                                                                                                                                            Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 LLHEWVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 VEETVSQDCNQDMEEMMSEQENPDSSEPV-VEDERLHHDTDDVTYQVYEEQAVYEPLENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----DRDADADRDGGDGDGVGYDYKDEEKG----TDSYKN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.7%; Score 188.5; DB 2; Length 792; Best Local Similarity 21.8%; Pred. No. 0.028; Matches 90; Conservative 58; Mismatches 147; Indels 117; Gaps
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                                                                                                                                                                                  C;Accession: T42963
*Ablacett, J.C.; Fleckenstein, B.
submitted to the EMBL Data Library, August 1998
A;Description: Primary structure of the herpesvirus ateles genome.
A;Reference number: Z22274
A;Accession: T42963
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                              - ateline herpesvirus 3 (strain 73)
                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-792 <ALB>
A;Cross-references: EMBL:AF083424; PIDN:AAC95573.1
A;Experimental source: strain 73
                                                     A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-706 <KNU>
                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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                         RESULT 11
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C;Accession: T08929

C;Accession: T08929

W.; Zimermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; May submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 345/3; 357/1; 384/3; 404/3; 441/3; 472/3; 500/3; 667/1; 697/3; 708/1
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313 EGEKKKAEKKVITETKKKAEKEDAKKKSEKETDIDMKKKEPGKSPDTKPGTVKVTTQAAT 372
                                                                                            350 KLRKRGKIEEAVNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVA 409
                                                                                                                                                                                             373 K--KDEKKEDSKKA-KKPAEEQPK-----GKKQ------EKKEKHE--EPAKSTKKEHA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 RSTSEPAVPPEEAEPHT------EPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVH 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T15N24.80 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.5%; Score 183; DB 2; Length 763;
Best Local Similarity 21.8%; Pred. No. 0.052;
Matches 126; Conservative 84; Mismatches 217; Indels 150; Gaps
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R;Mak, A.S.; Carpenter, M.; Smillie, L.B.; Wang, J.H. J. Biol. Chem. 266, 19971-19975, 1991 A,Title: Phosphorylation of caldeemon by p34 (cdc2) kinase. Identification of phosphorylat A,Feference number: A41064; MUID:92041815; PMID:1939059 A,Accession: A41064 A,Molecule type: protein A,Residues: 597-600;678-696;711-721 <mak> B,Amelocule type: protein A,Residues: 597-600;678-696;711-721 <mak> A,Title: Caldeemon has two calmodulin-binding domains. A,Reference number: A60461; MUID:89334885; PMID:2757638 A,Accession: A60461 A,Molecule type: protein A,Residues: 2-17, X, X, 19-38;466-485 <man> R;Haruna, M.; Havashi, K.; Yano, H.; Takeuchi, O.; Sobue, K.</man></mak></mak>	A; Title: Common structural and expressional properties of vertebrate caldesmon genes. A; Title: Common structural and expressional properties of vertebrate caldesmon genes. A; Reference number: PC2003; MUID:94071934; PMID:8250919 A; Recession: PC2003 A; Molecule type: DNA A; Residues: 74-419 e.HAR. B; Takagi, T: Yazawa, M:; Ueno, T:; Suzuki, S.; Yagi, K. J: Biochem. 106, 778-783, 1989 A; Title: Amino acid sequence studies on cyanogen bromide peptides of chicken caldesmon whe A; Reference number: PX0022; MUID:90130380; PMID:2613684 A; Reference number: PX0022	A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Residues: 462-47.0°, 479-563;674-762, 'A', 763-771 < TAK> C; Comment: This protein plays a vital role in the regulation of smooth muscle and nonmusc C; Comment: The binding of caldesmon to F-actin is modulated by calcium and calmodulin. C; Comment: Two calmodulin molecules can bind to nonoverlapping domains of each caldesmon. C; Superfamily: caldesmon C; Keywords: actin binding; alternative splicing; calmodulin binding; cytoskeleton; muscle F; 1-771/Forduct: h-caldesmon #status predicted <hmat> F; 1-318,334-711/Forduct: h-caldesmon, alternative splice form #status predicted <lmat> F; 26-390/Region: tropomyosin binding F; 511-582/Region: tropomyosin binding F; 522-665/Region: tropomyosin binding F; 522-665/Region: tropomyosin binding F; 582-665/Region: tropomyosin binding F; 582-71/Region: tropomyosin binding F; 588-71/Region: tropomyosin binding</lmat></hmat>	171; 18 174; Gaps 3AEPQNI	Db 515EKQQEAAVELDELKKRREERRKILEEEEQKKK 546
Qy 161 AEHVEGEDLOQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVS 204	Db 264 DEKEETNDDKEDERESKGSKRRR. Qy 368 VRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVASLPDVPADL 418 Db 306KKDAEPRTPFSDRPVRERKSVERLVALIDKDSSKEFRVEKGRGAYLKDIPNVA 358 Qy 419 LKLSLKRRSDRQQFLGHMRGSLLTLQRLVQLFPNDTSLKNDLGV-GYLLIGDNDN 472 Db 359 NKVMRKRSDFTKLLHPILEGGRRGKAAQIKTHILGFSGFVWHGDEKK 406 Qy 473 AKKVYEEVLSVTPNDGPAKVHYGFILKAQNKIAESIPYLKEGIESGDPGTDDG 525	407 AKEKVKEKLEKCTKEKLMEPCDVLDIHİTKATTKKEDIİTKLFEFLEKPHYTGDVTGD 464 526 RFYFHLGDAMQRYGNKEAYKWYELGHKRGHPASVWQRSLYNVNGLKAQPWMTPKETGYTE 585 465TTVSEKEKSSKGAKRRRTPKKTSPTA 490 586 LVKSLERNWKLIRDEGLAVMDKAKCIFLPEDENLREK 622 491 GSSSSKRSAKSQKKSEEATKVVKKSLAHSDDESEEEK 527 53430	lidesmon - chicken Letnate names: caldesmon, smooth muscle; calmodulin- and actin-binding protein Letnate names: caldesmon, smooth muscle; calmodulin- and actin-binding protein Lecises: 341us gallus (chicken) tte: 27-Reb-1990 #sequence revision 27-Jun-1994 #text change 22-Jun-1999 vashi, K.; Kanda, K.; Kimizuka, F.; Kato, I.; Sobue, K. then: Blophyse Res. Commun. 164, 503-511, 1989 vashi, K.; Kanda, K.; Mimizuka, F.; Kato, I.; Sobue, K. then: Blophyse Res. Commun. 164, 503-511, 1989 ference number: A33430 Jecule type: mRNA sidues: 1-71 cHAY. sidues: 1-71 cHAY. sidues: 1-77 cHAY. sidues: 1-77 cHAY. sidues: 1-71 cHAY. sidues: 1-319.34-771 cHRY. sidues: 1-	A;Residues: 466-771 <ha2> A;Cross-references: GB:M26684; NID:g211897; PIDN:AAA48811.1; PID:g211898</ha2>

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16;
                                                                                                    661 PVPAEGVRNIKSMWEKGNVFSSPGGTGTP---NKETAGLKVGVSSRINEWLTKTPEG--- 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 ----BALEELBEPQQAPAKAQPEAQPEGDI--AVEALBEL-EEPQQAPAEAQPEG 284
 ---LSVTPNDGFA---KVHYGFILKAQN-KIA 505
                                     547 QEEAERKIREEEEKKRMKBEIERRRAEAEKROKVPEDGVSEEKKPFKCFSPKGSSLKIE 606
                                                                                                                                                     ------HFASVWQR-SLYNVNGLKAQPWWTPKET-GYTELVKSLERNWKLIRDEGLAV 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 QQEDGPIGEPQQEDDEFLMATDVD-DRFETLE--PEVSHEETEHSYHVEETVSQDCNQDM 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEMMSEQENPDSSEP-VVEDERLHHDTDDVTYQVYEE-----QAVYEPLENEG--- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 IEITEVTAPPEDNPVE-----DSQVIVEEVSIFPVEEQQEVPPETNRKTDDPEQKAKV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 KKKKPKLINKFDKTIKAELDAAEKLRKRGKIEEAVNAFKELVRKYPQSPRARYGKAQCED 386
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                                                                                                                                                                                                                           605 MDKAKGLFLPEDENLREKGDWS-QFTLWQQGRRNENACKGAPKTCTLLEKFPETTGCRR 662
                                                                                                                                                                                                                                                     flagellar antigen - Trypanosoma brucei (fragment)
C;Species: Trypanosoma brucei
C;Date: 13-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 EELEEPQQAPAEAQPEALPEGDIAVEALBELEEPQQVPAEAQPEAVAPEGDIAVEALEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 411;
                                                                          506 ESIPYLKEGIESGDPGTDDGRFYFHLGDAMQRVGNK-EAYKWYELGHKRG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.5%; Score 179.5; DB 2; Length 25.1%; Pred. No. 0.036; tive 53; Mismatches 128; Indels
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Job time : 23 secs
460 LGVGYLLIGDNDNAKKVYEEV-
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GenCore version 5.1.6
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OM protein - protein search, using sw model

May 5, 2004, 10:56:23 ; Search time 18 Seconds (without alignments) 2192.732 Million cell updates/sec Run on:

US-09-903-216-2 4022 1 MAQRKDAKSSGNSSSSGSGS.....IVDVWHPELTPQQRRSLPAI 758 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q12797 homo sapien	bos t	_	Q8t5t1 giardia lam	-		orycto.		homo sa		Q92794 homo sapien	P53935 saccharomyc		P31569 oenothera v	P21619 mus musculu			Q10411 schizosacch	P38911 saccharomyc	Q05682 homo sapien		O60841 homo sapien		Q02224 homo sapien		P31568 oenothera p	Q01484 homo sapien	0	O60184 schizosacch	P21127 homo sapien	Q9uq88 homo sapien	homo	CHC.H
SUMMERTES		ASPH HUMAN	ASPH_BOVIN	TRDN CANFA	MDN1 GIALA	ECX1 METMA	P200 MYCGE	TRDN RABIT	CALD CHICK	TRDN HUMAN	NFM RAT	MYS3 HUMAN	YNJ1 YEAST	YHU6 YEAST	YCF2 OENVI	LAM2 MOUSE	YFI6 YEAST	NUCL_XENLA	SPOF SCHPO	FKB3 YEAST	CALD HUMAN	NFM MOUSE	IF2P HUMAN	SP41 YEAST	CENE HUMAN	MDN1 YEAST	YCF2 OENPI	ANK2 HUMAN	RASO METTH	YG49 SCHPO	CDL1 HUMAN	CDL2 HUMAN	KIN1 HUMAN	NPI.3 HIMAN
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	Query Match Length	757	754	700	4835	493	1616	705	771	728	845	2004	1240	465	630	592	1233	. 650																
o¥.		98.6		5.0	4.8	4.8	4.7	4.6	4.5	4.4	4.4	4.4	4.3	4.3	4.3	4.2	4.2	4.1	4.1	4.1	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	3.9	3.9	9.8	3.9	3.9	6
	Score	3966.5	3172	203	194	193	189.5	187	181	178.5	176.5	175	172.5	172	172	169.5	169.5	165	164	163	162.5	161.5	161.5	161.5	161	161	160.5	159	158.5	158.5	158	157.5	157.5	756 5
	Result No.		8	3	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q03661 Baccharomyc	P22793 Ovie aries	Q07283 homo sapien	P36080 saccharomyc	Q12114 saccharomyc	057521 brachydanio	P11501 gallus gall	Q9r0x5 mus musculu	097593 bos taurus	Q14683 homo sapien	Q14692 homo sapien
YM67_YEAST	TRHY SHEEP	TRHY HUMAN	YKI2 YEAST	CHS5_YEAST	HS9B_BRARE	HS9A_CHICK	RPGR MOUSE	SM1A BOVIN	SM1A HUMAN	BMS1_HUMAN
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156.5	154.5	153.5	152	152	152	152	152	152	152	152
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        661 RRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETRTWEEGKVLIFD 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLAVMDKAKGLFLPEDENLREKGDWSQFTLWQQGRRNENACKGAPKTCTLLEKFPETTGC
                                                                                                                                                                                                                                                                                                                                                         1 MAQRKNAKSSGNSSSSGSGSGSTSAGSSSPGARRETKHGGHKNGRKGGLSGTSFFTWFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 QEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 PVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPVEEQQEVPPETNRKTDDPEQKAKVKKKRPKLLNKFDKTIKAELDAAEKLRKRGKIEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 VNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVASLPDVPADLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSLKRRSDRQQFLGHMRGSLLTLQRLVQLFPNDTSLKNDLGVGYLLIGDNDNAKKVYEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSLKRRSDRQQFLGHMRGSLLTLQRLVQLFPNDTSLKNDLGVGYLLIGDNDNAKKVYEEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 KEAYKWYELGHKRGHFASVWQRSLINVNGLKAQP-CGPKETGYTQLVKSLERNWKLIRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601 GLAVMDKAKGLFLPEDENLREKGDWSQFTLWQQGRRNENACKGAPKTCTLLEKFPETTGC
                                                                                                                                                                                                                                                                                                                                                                              1 MAQRKNAKSGUSSSSGSGSGSTSAGSSPGARRETKHGGHKWGRKGGLSGTSFFTWFWV
                                                                                                                  SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                         Gaps
             InterPro; IPR001440; TPR.
Pfam; PF05279; Asp-B-Hydro N; 1.
Pfam; PF05118; Asp-B-Hydro N; 1.
Oxidoreductase; Dioxygenase; Iron; Transmembrane; Signal-anchor; Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                        POLY-LYS.
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                  98.6%; Score 3966.5; DB 1; Length 757; 99.2%; Pred. No. 3.4e-193;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (PC
1A79313A4934C430 CRC64;
                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI 758
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                                                                                                                                                          LUMENAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                            POLY-SER.
InterPro; IPR008940; Prenyl_trans.
                                                                                                                                                                                                                               705 N
85498 MW;
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                       54
75
                                                                                                                                                                                                                                                                                                      Similarity
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nes 752;
                                                                                                   DOMAÎN
TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                          DOMAIN
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PTM: Might be processed to the 56 kDa (AA 289-754) or 52 kDa (AA 311-754) forms in the lumen of the endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: Peptide L-aspartate + 2-oxoglutarate + O(2) peptide 3-hydroxy-L-aspartate + succinate + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Bovine liver aspartyl beta-hydroxylase. Purification and characterization.";
J. Biol. Chem. 266-14004-14010(1991).
-!- FUNCTION: Specifically hydroxylates an Asp or Asn residue in certain epidermal growth factor-like (EGF) domains of a number
                                                                                                                                                                                                                                                                                TISSUE=Brain, and Liver;
MEDLINE=92332546; PubMed=1378441;
Jia S., Vandusen W.J., Diehl R.E., Kohl N.E., Dixon R.A.F.,
Jis S., Vardusen W.J., Friedman P.A.;
"CDNA cloning and expression of bovine aspartyl (asparaginyl) beta-
                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A42969; BABOH.
InterPro; IPR007943; Asp-B-hydro N.
InterPro; IPR007803; Asp_Arg_Hydrox.
InterPro; IPR008941; TPR-like.
InterPro; IPR001440; TPR-like.
Pfam; PF05279; Asp-B-Hydro N; 1.
Pfam; PF05118; Asp_Arg_Hydrox; 1.
Cxidoreductase; Dioxygenase; Iron; Transmembrane; Signal-anchor; Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang Q., Vandusen W.J., Petroski C.J., Garsky V.M., Stern A.M., Friedman P.A.;
                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
11-NAR-2004 (Rel. 43, Last annotation update)
Aspartyl/asparaginyl beta-hydroxylase (BC 1.14.11.16) (Aspai hydroxylase) (ASP beta-hydroxylase) (Peptide-aspartate beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LUMENAL (POTENTIAL)
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POLY-LYS.
N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                    hydroxylase.";
J. Biol. Chem. 267:14322-14327(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91310689; PubMed=1856229;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 289-385 AND 615-641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M91213; AAA03563.1; -.
                 STANDARD:
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12
21
21
328
96
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78
                                                                                                                                                                                                                    Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: Iron.
-!- SUBUNIT: Monomer.
                                                                                                                                                                   Bos taurus (Bovine).
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   NCBI_TaxID=9913;
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                                                                                                                                  dioxygenase)
                 BOVIN
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DOMAIN
CARBOHYD
CARBOHYD
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ASPH BOVIN
ID ASPH BOV
AC Q28056;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   577 IGYTELVKSLERNWKLIRDEGLAAMDRTHGLFLPEDENLREKGDWSQFTLWQQGRKNENA 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKGAPKTCTLLEKFPETTGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGC 700
                                                                                                                                                                                                                                                 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKAELDAAEKLRKRGKIEEAVNAPKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRG 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVGYLLIGDNDSAKKVYEEVLSVTPNDGFAKVHYGFILKAQNKIABSIPYLKEGIESGDP 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTDDGRFYFHLGDAMQRVGNKEAYKWYELGHKRGHFASVWQRSLYNVNGLKAQPWWTPKE 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTDDGRFYFHLGDAMQRVGNKEAYRWYELGHQRGHFASVWQRSLYNVQGLKAQPWWTPKE 576
                                                                                                                                                                                                                                                                                          61 FMVIALLGVWTSVAVVWFDLVDYEEVLAKAKDFRYNLSEVLOGKLGIYDADGDGDFDVDD 120
                                                                                                                                                                                                                                                                                                                                    103 AKVLLGLKERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 NQDMEEMMSEQENPDSSEPVVED--ERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVT 280
                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     701 KIRCANETRIWEEGKVLIFDDSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               697 KIRCANETRTWEEGKVLIFDDSFEHEVWQDAASFRLIFIVDVWHPELTPHQRRSLPAI 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       637 CKGAPKTCSLLDKFPETTGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGC
                                                                                                                                                                                                                                                                                                                                                                                                                            163 HVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      --PGENLPQEPEGPAEELQPDDHVFVGSDADDRYEPMGTGAVHEETEDSXHIBETASPAY
                                                                                                                                                                                                  1 MAPRICHAKGGGGNSSSSSSSSPTGCTSGGSSSPGARRETKQGGLKNGRKGGLSGSSFFTW
                                                                                                                                                                                                                                                 -GKLGIYDADGDGDFDVDD
                                                                                                                                                                                                                                                                                                                                                                                121 AKVLLGLKEKPAPKPTVPPEEADMYPWLEDQVLESPGRQNIEDEVYEQVQS-LDETVYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 APPEDNPVEDSQVIVEEVSIFPVEEQQEVPPETNRKTDDPEQKAKVKKKKPKLLNKFDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIETYQEVASLPDVPADLLKLSLKRRSDRQQFLGHMRGSLLTLQRLVQLFPNDTSLKNDL
                                                                                                                                                         1 MAQRKNAKSSG---NSSSSGSGSGSGSTSAGSSSPGARRETXHGGHKNGRKGGLSGTSFFTW
                                                                                                               Gaps
                                                                                                             44;
702 702 N-LINKED (GLCNAC. . .) (POTENTIAL) 754 AA, 84998 MW, 369593A1F0B558C8 CRC64;
                                                                   Length 754;
                                                                                                             77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 78.9%; Score 3172; DB 1; Best Local Similarity 78.7%; Pred. No. 4.2e-153; Matches 612; Conservative 45; Mismatches 77;
                                                                                                                                                                                                                                                   58 FMVIALLGVWTSVAVVWFDLVDYEEVL --
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                         SEQUENCE
    CARBOHYD
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RESULT 3
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ID TRON CANFA
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AC P82179;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Triadin.
DE Triadin.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TAXID=9615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 GFFSLLSDIISSDGDEDDDDGDEDTDKGEI----EEPPLKQKEIHKEKAEKEEKPERKIL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VSP_004003.
EEVVYQQVÄTEKADIEKTVKPKPAKKAEHQEKESPTIKTD
EEVVYQVÄTEKADIEVOS
ELVOVDVVINLIFLVOPQOD
ELNVESKVFRMIHVLSHPTSRTSPILVISTTCRT (in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----WLLVIALIITWSAVAVWMFDLVDYKNFSASSLSKIGSDPLKLVHDAVEETTDWVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 NAKSSGNSSSSGSGSGSTSAGS-----SPGARRETKHGGHKNGRKGGLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                   expressed in mammalian myocardium.",
J. Biol. Chem. 274:28660-28668(1999).
-!- FUNCTION: May be involved in anchoring calsequestrin to the junctional sarcoplasmic reticulum and allowing its functional coupling with the ryanddine receptor (By similarity).
-!- SUBCELLULAR LOCATION: Type II membrane protein. Sarcoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F -> EPIKĞKEVKVPGSLKEKE (in isoform
Cardiac 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.0%; Score 203; DB 1; Length 700;
19.3%; Pred. No. 0.0027;
tive 95; Mismatches 236; Indels 258;
                                                        Kobayashi Y.M., Jones L.R.; "Identification of triadin 1 as the predominant triadin isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 TSFFTWFMVIALLGVWTSVAVVWFDLVDYEEV----LGKLG-----IYDA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (in isoform Cardiac 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKQIQ (in isoform Cardiac 1). /FTId=VSP 004001.
                                                                                                                                                                                                                                                                                                                 VSP 004004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F033E3AA1BEE0C56 CRC64;
                                                                                                                                                                                                                                                                                   IsoId=P82179-2; Sequence=VSP_004001, VSP_004002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF165916; AAF00222.1; -.
EMBL; AF165915; AAF00221.1; -.
EMBL; AF165917; AAF00223.1; -.
Transmembrane; Sarcoplasmic reticulum; Glycoprotein;
Alternative splicing.
                                                                                                                                                                                                                                                                                                                 IsoId=P82179-3; Sequence=VSP_004003, VSP_00400
TISSUE SPECIFICITY: Skeletal and cardiac muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOYAFCRYMIDMFVHGDLRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isoform Cardiac 3).
                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTIG=VSP 004002
         SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
TISSUE=Heart, and Skeletal muscle;
MEDLINE=99428545; PubMed=10497235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                                                    IsoId=P82179-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                   -!- ALTERNATIVE PRODUCTS:
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700
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                                                                                                                                                                                                                                                                      Name=Cardiac 1;
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                                                                                                                                                                                                                                      Name=Skeletal;
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Matches 141;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 630 DLEDVSASKKAKEEAEDVSSTKRQKSPISFFQCVYLDGYNGYGFQFPV-----TPAYR 682
                                                                                                                                                                                                                                                                                                                         395 YVEPAKSSKKEHSAPSEKQVKAKTERAKEETSAASTKKAVPGKKEEKTTKTVEQEI---- 450
                                                                                                                                                                                                                                                                                                                                                             --EEAVNAFKELVRKYPQSPRARYGK-----AQCEDD 387
                                                                                                                                                                                                                                                                                                                                                                                                                                     -----TYQEVASLPDVPADLLKLS 422
                                                                                                                                                                            275 RPGOSPALPPPLPTVQASRPTPASPTLEGKEEEEKKKKAEKKVTSETKKKEKEDVKKKSDK 334
                                                                                                                                                                                                                                        : |: | | :: ||
335 DTAIDVEKKEPGKAPETKQGTIKVVAQAAAKKDEKKEDSKKTKTPVEHPKGKKQEKKEK 394
                                                                                                                                                                                                                                                                                     309 -VPPETNRKTDD--PEQK-------AKVKKKKP-KLINKFDKTIKAELDAAE 349
                                                                                                                                                                                                                                                                                                                                                                                               451 RKEKSGKTSTASKDKEPEIKKDERMPKADKEVKPROPOSQVKKEEKSESQVKKEAKPEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                          570 SKETPEVTESGKKKIEKSEKESKEKAEMKHLKEEKVSTRKESLQSHNVTKAEKPARVSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               466 LIGDNDNAKKVYEEVLSV-----TPNDGFAKVH-----YGFILKAQNKIAESIPYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garbarino J.E., Gibbons I.R.;
"Expression and genomic analysis of midasin, a novel and highly conserved Ash protein distantly related to dynein.";
BMC Genomics 3:18-18(2002)
-:- FUNCTION: May function as a nuclear chaperone and be involved in the assembly/disassembly of macromolecular complexes in the
                                                                       --HEETEH----SYHVEETVSQDC
                                                                                            VEA---EPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDV
                        160 AKVAHREKEKVYEKEKSE----KKATHKEKIEKKEKPETKTMAKEERKAKTEEKIKKEV
                                                                                                                                           -----SEQENPDSSEPVVEDERLHHDTDDVTYQVYE
                                                                                                                                                                                                               --yepleneg-ieitevtappednpvedsqviveevsifpveeqge----
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IDENTIFICATION, GENE NAME, AND SIMILARITY WITH OTHER FAMILY MEMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCARTHUR A.G., Morrison H.G., Nixon J.E., Passamaneck N.Q., Kim U., Hinkle G., Crocker M.K., Holder M.E., Farr R., Reich C.I., Olsen G. Aley S.B., Adam R.D., Gillin P.D., Sogin M.L.; "The Giardia genome project database.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Diplomonadida, Hexamitidae, Giardiinae, Giardia.
NCBI_TaxID=5741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 41, Last sequence update) (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 4835 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ----NEVLRGAIE--
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                                                                                                                                               223 NQDMEEMM-----
                                                                       193 -DDRFETLEPEVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                       388 LAEKRRS----
                                                                                                                                                                                                                                                                                                                                                               350 KLRKRGKI---
                                                                                                                                                                                                                   262 EQAV-----
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SEQUENCE FROM N.A.
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23.1%; Pred. No. 0.084;
Ive 74; Mismatches 203; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539726 MW; 3A9E12417DB04A50 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AF494287; AAM12656.1; -.
InterPro; IPR0013593; AAA ATPAse.
InterPro; IPR0013959; AAA ATPAse_centr.
InterPro; IPR002035; WWF.A.
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Matches 119; Conservative 7
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ECX1 METMA RESULT 5

SIMILARITY: Contains 1 VWFA domain.

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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
     440 EAEABBEAE--PEVEAEEISTEAEEAEEPEEE---KSEGPW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 256-427; 432-543 AND 1083-1140 FROM N.A.
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tive 78; Mismatches 205;
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S -> F (IN REF. 2).
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2 X 26 AA REPEAT.
2-1.
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                                                                                                                                                                                          Q49429; Q49259; Q49298; Q49352; Q49353;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-FBB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOT ANNOTATED CDS.
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                                                351 LRKRGKIEE
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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304
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DOMAIN 120
                                                                                                                                                                                                                                                                     Protein P200.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 -----GLKERSTSEPAV-----PPEEAEPHTEPE-----EQVPVEAEPQ 141
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=GOel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
STRAIN=22120827; PubMed=12125824;
MEDLINE=22120827; PubMed=12125824;
MEDLINE2-Axias R., Henne A., Hartsch T., Merkl R., Schmitz R.A.,
Martinez-Axias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,
Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Fritz H.-J., Gottschalk G.;
The genome of Methanosarcina mazei: evidence for lateral gene
transfer between Bacteria and Archaea.";
                                                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Microbiol. Biotechnol. 4:453.461(2002).
-!- FUNCTION: Probably involved in the 3'->5' degradation of a variety of RNA species (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 ELKEFDEIEARL--EKEDASIEAEEEIEPEAERATEEGLEEEA-EIEETAASEEEN-IEA
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Pfam; PF01138; RNase_PH; 1.
Pfam; PF01128; RNase_PH C; 1.
Exosome; Hydrolase; Ruolase; Exonuclease; Complete proteome.
DOMAIN 1 254
PROBABLE EXOSOME COMPLEX EXONUCLEASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDV---DDAKVLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.8%; Score 193; DB 1; Length 493; 26.3%; Pred. No. 0.0056; tive 45; Mismatches 129; Indels
                                                                                                                                         Archaea, Buryarchaeota, Methanomicrobía, Methanosarcinales,
Methanosarcinaceae, Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: Component of the archaeal exosome multienzyme ribonuclease complex (Potential).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Belongs to the RNase PH family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         979A757BEF8DC090 CRC64;
                                                    10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable exosome complex exonuclease 1 (EC 3.1.13.-).
                                                                                                                            Methanosarcina mazei (Methanosarcina frisia)
493 AA
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PRT;
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                                    (Rel. 42, Created) (Rel. 42, Last seg
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 STANDARD;
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                                                                                                                                                                                NCBI TaxID=2209;
                                    10-0CT-2003
 ECX1 METMA
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---KVVKDPSEAG-- 486
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MEDLINE=96026346; PubMed=756993;
MEDLINE=96026346; PubMed=756993;
Praser C.M., Goodyne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Fritchman D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
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22.3%; Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 33530 / G-37;
MEDLINE=94075230; PubMed=8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Structural protein; Repeat; Complete proteome.
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1211 SQPEATFD--TVQPEQTPQE----AKFDSPVETVEQPEFSSEPTQQ--HVESEASFDEPN 1262
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                                                                             1091 FÖTVKHEAVFDKNQTQTEGLEBPQVSSEAEVVDQTTTDTVGEPEAVFDVQPEKTTEVKFD 1150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270 ENEGIEITEVTAPPE-DNPVE---DSQ--VIVEEVSIFPVEEQQEVPPETNRKTDDPEQK 323
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                                                                                                                                                                                                                                                                                                                            166 GEDLOQEDGPTGEPQQEDDEFLMATDVDDRFETLE-PEVSHEETEHSYHVEETVSQD-CN 223
FDLVDYEEVLGK------LGIYD-----ADGDGDFDVDDAKVL---- 106
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Knudson C.M., Stang K.K., Moomaw C.R., Slaughter C.A., Campbell K.P.;
"Primary structure and topological analysis of a skeletal muscle-
Specific junctional sarcoplasmic reticulum glycoprotein (triadin).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  499 KAQ--NKIAESIPYLKEGIESGDPGTDDGRFYFHL-GDAMQ-RVGNKEAYKWYELGHKRG
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                                                                                                                                                           107 -LGLKERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVE
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Peng M., Fan H., Kirley T.L., Caswell A.H., Schwartz A.;
"Structural diversity of triadin in skeletal muscle and evidence of
its existence in heart.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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30-MMX-2000 (Rel. 39; Created)
10-OCT-2003 (Rel. 39; Last sequence update)
10-OCT-2003 (Rel. 42; Last annotation update)
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DQYAFCRYMĪDIFVHGDLKPGQSPAIPPPSPTEQASRPTPA
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GQHAFCLKGC (in isoform Cardiac 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isold=028820-5; Sequence=VSP 004462, VSP_004463, VSP_004464, VSP_04465;
                                                                                                                                                                                        Fan H., Brandt N.R., Caswell A.H.;
"Disulfide bonds, N-glycosylation and transmembrane topology of skeletal muscle triadin.";
Biochemistry 34:14902-14908(1995).
-!- FUNCTION: May be involved in anchoring calsequestrin to the junctional sarcoplasmic reticulum and allowing its functional coupling with the ryanodine receptor.
-!- SUBUNIT: Homooligomer of variable subunit number; disulfide-
                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Type II membrane protein. Sarcoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .).
                                                                                            cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (In isoform Cardiac 2). /FIId=VSP_004461.
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          [3]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORMS CARDIAC)
TISSUB-Heart muscle;
MEDLINE-96132942; PubMed-8550602;
Guo W., Jorgenen A.O., Jones L.R., Campbell K.P.;
"Biochemical characterization and molecular cloning of card.
                                                                                                                                                           CARBOHYDRATE-LINKAGE SITES, AND INTERCHAIN DISULFIDE BONDS.
MEDLINE=96066664; PubMed=7578102;
                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Skeletal 1; Synonyms=ST1;
IsoId=Q28820-1; Sequence=Displayed;
Name=Cardiac 1; Synonyms=CT1;
IsoId=Q28820-2; Sequence=YSP_004458, VSP_004460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Cardiac 2; Synonyms=CT2; IsoId=Q28820-3; Sequence-VSP_004459, VSP_004461; Name=Cardiac 3; Synonyms=CT3; IsoId=Q28820-4; Sequence-VSP_004466; IsoId=Q28820-4; Sequence-VSP_004466; Name=Skeletal 2; Synonyms=ST2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Skeletal 3; Synonyms=ST3;
IsoId=Q28820-6; Sequence=VSP 004464; VSP 004465;
-:- TISSUB SPECIFICITY: Skeletal and cardiac muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Sarcoplasmic reticulum; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=6;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          004460.
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                                                                                                          triadin.";
J. Biol. Chem. 271:458-465(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U31540; AAC48496.1; --.
EMBL; L10066; AAA31488.1; --.
EMBL; U31555; AAC48497.1; --.
EMBL; U34201; AAC48498.1; --.
FEBS Lett. 348:17-20(1994)
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67
705
74
624
624
285
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254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 KLRKRGKIEBAVNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVA 409
                                                                                                                                                                                                                                                                                                                                                                                                               93 ------DGDGDFDVDDAKVLLG-LKERSTSEPAVPPEEAEPHTEPEEQVPV--- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 GFFSLLSDIISSDGDEEDDEGDEDTAKGEIEEPPLKRKDIHKEKIEKQEKPERKIPTKVV 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----EAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 HKEKEKEKEKVKEKEKPE-----KKATHKEKLEKKEKPETKTVTKEEKKARTK----- 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 DDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 DDVIYQVYEEQAVY----EPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQ 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 AAVSKOEOKDOYAFCRYMIDIFVHGDLKPGOSPAIPPPSPTEOAS----RPTPALPTPEK 311
                                                                                                                                                                                                                                                                                                                          6 NAKSSGNSSSSGSGSGSTSAGS-----SSPGARRETKHGGHKNGRKGGLSG 51
                                                                                                                                                                                                                                                                                                                                                         48
                                                                                                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                          TPAQYPGESSGKPNSPGPKQ -> LLATVGIWGMNQWMEDL
SVTLPSK (in isoform Cardiac 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 ----EKIEBKTKKE------KKGVKOEKVKQTVAKAKEVQKTPKPK-----EKESKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                             D \rightarrow E (in isoform Skeletal 2 and isoform
                                                                                                                                                            SKKAKEEAEEVSSTKKOKSPISFFOCVYLDGYNGYGFQFPV
                                                                                                                                                                                                                                                                                                                                                                                       52 TSFFTWFMVIALLGVWTSVAVVWFDLVDYEEV----LGKLG-----IYDA-----
                                                                                          /FIIG-VSP_004464.
Missing (in isoform Skeletal 2 and isoform Skeletal 3).
                                                                                                                                                                                                                                                      4.6%; Score 187; DB 1; Length 705;
21.0%; Pred. No. 0.018;
tive 77; Mismatches 165; Indels 152;
               P 004462.
(In isoform Skeletal 2)
-> E (in isoform Skeletal 2).
                                                                                                                                                                                                                             13AF1D84475A1361 CRC64;
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                                                                                                                                                                                                            /FTId=VSP 004466
                                                                                                                                             FTId=VSP_004465
                                               004463
                                                                              Skeletal 3)
                                             /FTId=VSP
               FTId=VSP
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                                                                                                                                                                                                                              705 AA; 79003 MW;
                                                                                                                                                                                                                                                                                           Conservative
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 415
                                  424
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                                                                                                                                                               645
 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137
                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                               Query Match
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORM GIZZARD H-CAD).

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Mang Z., Danielsen A.J., Mainle N.J., McManus M.J.;
Warng Z., Danielsen A.J., Mainle N.J., McManus E.J.;
"Tyrosine phosphorylation of caldesmon is required for binding to the Shc.Carb complex."
J. Biol. Chem. 274:33807-33813(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashi K., Yamada S., Kanda K., Kimizuka F., Kato I., Sobue K., Hayashi K., Parada S., Kanda K., Kimizuka F., Kato I., Sobue K., S. & Raguente of h-caldesmon conserves two consensus sequences of the tropomyosin-binding domain in troponin T.";

Biochem. Biophys. Res. Commun. 161:38-45 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=92041815; PubMed=1939059;
Mak A.S., Carpenter M., Smillie L.B., Wang J.H.;
"Phosphorylation of caldesmon by p34cdc2 kinase. Identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yano H., Hayashi K., Haruna M., Sobue K.; ^{\prime} "Identification of two distinct promoters in the chicken caldesmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mornet D., Audemard B., Derancourt J.; "Identification of a 15 kilodalton actin binding region on gizzard
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (GIZZARD H-CAD; BRAIN L-CAD AND GIZZARD L-CAD).
                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORM GIZZARD H-CAD)
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORM BRAIN L-CAD)
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE-94071934; PubMed-8250919; Haruna M., Hayashi K., Yano H., Takeuchi O., Sobue K.; "Common structural and expressional properties of vertebrate
                                                                                                                                                              Hayashi K., Kanda K., Kimizuka F., Kato I., Sobue K.; "Primary structure and functional expression of h-caldesmon complementary DNA.";
                                   Bryan J., Imai M., Lee R., Moore P., Cook R.G., Lin W.-G.; "Cloning and expression of a smooth muscle caldesmon."; J. Biol. Chem. 264:13873-13879(1989).
                                                                                                                                                                                                                                                                                                   MEDIINE=91093148; PubMed=1824698;
Hayashi K., Fujio Y., Kato I., Sobue K.;
"Structural and functional relationships between h- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 451-756 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene.";
Biochem. Biophys. Res. Commun. 201:618-626(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-15 FROM N.A. (ISOFORM BRAIN L-CAD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caldesmon probed by chemical cross-linking.";
Biochem. Biophys. Res. Commun. 154:564-571(1988)
                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 164:503-511(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem, Biophys. Res. Commun. 197:145-153(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence of an avian non-muscle caldesmon.";
J. Muscle Res. Cell Motil. 12:372-375(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM GIZZARD L-CAD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION OF TYR-27 AND TYR-165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Biol. Chem. 266:19971-19975(1991).
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MEDLINE=94271210; PubMed=8002994;
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                                                                                                                                                    MEDLINE=90026426; PubMed=2803315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Gizzard;
MEDLINE=92042686; PubMed=1939602;
TISSUB-Gizzard, and Oviduct;
MEDLINE-89340480; PubMed-2760048;
                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 266:355-361(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caldesmon genes.";
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                                                                                                                                                                                                                                                                                                                                                                 1-caldesmons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Gizzard;
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regulation of actomyosin interactions in smooth muscle and
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EMBL;
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EMBL;
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EMBL;
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filaments). Stimulates actin binding of tropomyosin and actin filaments). Stimulates actin binding of tropomyosin which increases the stabilization of actin filament structure. In muscle tissues, inhibits the actomyosin Afrase by binding to F-actin. This inhibition is attenuated by calcium-calmodulin and is potentiated by tropomyosin. Interacts with actin, myosin, two molecules of tropomyosin and with calmodulin. Also play an essential role during callular mitosis and receptor capping. SUBCELLULAR LOCATION: On thin filaments in smooth muscle and on stress fibers in filaroblasts (nonmuscle) (By similarity).
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ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;

Name=Gizzard h-cad; IsoId=P12957-1; Sequence=Displayed;

IsoId=P12957-2; Sequence=VSP_004152, VSP_004153; Name=Gizzard 1-cad; Name=Brain 1-cad;

Isoid=P12957-3; Sequence=VSP_004153; TISSIB SPECIFICITY: High-molecular-weight caldesmon (h-caldesmon) is predominantly expressed in smooth muscles, whereas low-molecular-weight caldesmon (l-caldesmon) is widely distributed in non-muscle tissues and cells. Not expressed in skeletal muscle or

DOMAIN: The N-terminal part seems to be a myosin/calmodulin-binding domain, and the C-terminal a tropomyosin/actin/calmodulin-binding domain. These two domains are separated by a central helical region in the muscle forms.

PTM: Phosphorylated in non-muscle cells. Phosphorylation by Cdc2 during mitosis causes caldesmon to dissociate from microfilaments. Phosphorylation reduces caldesmon binding to actin, myosin, and calmodulin as well as its inhibition of actomyosin ArPase activity. Phosphorylation also occurs in both quiescent and dividing smooth muscle cells with similar effects on the interaction with actin and calmodulin and on microfilaments reorganization (By similarity). SIMILARITY: Belongs to the caldesmon family.

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JOINED. JOINED. JOINED. JOINED. JOINED.
JOINED. JOINED. JOINED. JOINED. JOINED. JOINED BAA04538.1; JOINED. BAA04538.1; JOINED. JOINED JOINED JOINED EMBL, J04968; AAA49067.1; -. EMBL, D17648; BAAA4539.1; -. EMBL, D17634; BAAA04539.1; J01EMBL, D17636; BAA04539.1; J01 D17637; BAA04539.1; D17638; BAA04539.1; D17639; BAA04539.1; D17639; BAA04539.1; D17640; BAA04539.1; D BAA04538.1; BAA04538.1; D17645; BAA04538.1; BAA04538.1; BAA04538.1; BAA04538.1; BAA04538.1; BAA04539.1; BAA04539.1; BAA04539.1; AAA48810.1; BAA04539.1 BAA04539.1 AAA48936.1 BAA04538.1 BAA04538.1 BAA04539.1 D17648; I D17642; D17643; D17646; M28417; D17644; M60620; D17636; D17637; D17639; D17644; D17641; D17645;

345 ERAKAE-----EERKAAEERAKAEKERKAAEERERAKAEEEKRAAEEKARLEAEKL 395

------RKRGKIEE-AVNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLR 399

---KIDDPEQKAKVKKKKPKLLNKFDKTIKAELDA----AEKL----

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352

GAIETYQEVASLPDVPADLLKLSLKRRSDRQQFLGHMRGSLLTLQRLVQLFPNDTSLKND 459

515 ---EKQQEAA----VELDELK---KRREERRKIL------

456 APKEEMKSVWDRKRGVPEQKAQNGERELTTPKLKSTENAFGRSNLK-GAANAEAGSEKLK 514

----EEEEQKKK 546

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108 GLKERSTSE----PAVPPEE----AEPHTEPEEQV-----PVEAE-----PQNI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 EDEAKEQIQSLIHEMVHAEHVEGEDLQ-QEDGPTGEPQQEDDEFLMATDVDDRFETLEPE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 TDAADKEKEEAEKEREKLEAEEKERLKAEEEKKAAEEKOKAEEEKKAAEERKAKAEEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 RAABERERAKAEEE----KKAAEERERAKAEEERKAAEERAKAEEER------KAAE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 GKKEEKDSEEEKPKEVPTEENQVDVAVEKSTDKEEVVETKTLAVNAENDTNAMLEGEGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 VSHEETEHSYHVEETVSQDCNQDMEENMSEQENPDSSEPV-VEDERLHHDTDDVTYQVYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYOSIN AND CALMODULIN-BINDING.

10 X 13 AA APPROXIMATE TANDEM REPEATS.

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SENTWS; PR01076; CALDESMON.
Muscle protein; Actin-binding; Calmodulin-binding; Phosphorylation;
Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 EQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPETNR
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; Pred. No. 0.039;
87; Mismatches 248; Indels 174;
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TROPOMYOSIN-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006017; Caldesmon.
InterPro; IPR006018; Caldesmon_LSP
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                                                                                                               BAA04540.1;
BAA04540.1;
BAA04540.1;
BAA04538.1;
BAA04538.1;
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D17637; B
D17639; B
                                            D17648;
D17634;
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D17641;
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                               QEBABRKIREEEBEKKRMKEEIBRRRAEAAEKRQKVPEDGVSEEKKPFKCFSPKGSSLKIE 606
                                                                                                    ERAEFLNKSAQK-----SGMKPAHTTAVVSKIDSRLEQYTSAVVGNKAAKPAKPASDL 660
                                                                                                                                                               661 PVPAAEGVRNIKSMWEKGNVFSSPGGTGTP---NKETAGLKVGVSSRINEWLTKTPEG--- 714
460 LGVGYLLIGDNDNAKKVYEEV-----LSVTPNDGFA---KVHYGFILKAQN-KIA 505
                                                                                                                                       555 -----HFASVWQR-SLYNVNGLKAQPWWTPKET-GYTELVKSLERNWKLIRDEGLAV 604
                                                                                                                                                                                                                                      and its localisation to chromosome 6q22-6q23.";

Eur. J. Blochem. 233:258-265(1995).

-!- FUNCTION: May be involved in anchoring calsequestrin to the junctional sarcoplasmic reticulum and allowing its functional coupling with the ryanodine receptor (By similarity).

-!- SUBUNIT: Homooligomer of variable subunit number; disulfide-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Skeletal muscle;
MEDLINE=96061957; PubMed=7588753;
Taske N.L., Eyre H.J., O'Brien R.O., Sutherland G.R., Denborough M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning of the cDNA encoding human skeletal muscle triadin
                                                                                                                                                                                                              605 MDKAKGLFLPEDENLREKGDWS-QFTLWQQGRRNENACKGAPKTCTLLEKFPETTGCRR
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type II membrane protein. Sarcoplasmic
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N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                  ESIPYLKEGIESGDPGTDDGRFYFHLGDAMQRVGNK-EAYKWYELGHKRG-
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INIT MET 0 0 BY SIMILARITY.
DOMAĪN 1 46 CYTOPLASMIC.
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(Rel. 39, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                        728 AA
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GO; GO:0006936; P:muscle contraction; TP
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Genew; HGNC:12261; TRDN.
                                                                                                                                                                                                                                                                                                                                        STANDARD;
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10-OCT-2003
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4.4%; Score 178.5; DB 1; Length 728;

Query Match

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                                                                                                                                                                                                          104 GFFSLLSDIISSEDEBDDBDBDTDKGEI----DEPPLRKKEIHKDKTEKQEKPERKIQT 159
                                                                                                                                                                                                                                                                           160 KVTHKE-KEKGKEKVRE--KEKPEKKATHKEKIEKKEKPETK------TVAKEQK 205
                                                                                                                                                                                                                                                                                                                        197 ETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERL----HHDT 252
                                                                                                                                                                                                                                                                                                                                                      206 KAKTAEKSEEKTKK--EVKGGKQEKVKQTAAKVKEVQKTPSKPKEKEDKEKAAVSKHEQK 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---SSPGARRETKHGGHKNGRKGGLSG 51
                                                                                                                                     137 BAEPQNIEDBAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRF
                                                                                                                                                                                                                                                                                                                                                                                         ----EEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kelly B.W., Gillespie C.S., Sherman D.L., Brophy P.J.; "Schwann cells of the myelin-forming phenotype express neurofilament
                 Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=87282618; PubMed=2441012;
Mapolitano E.W., Chin S.S.M., Collan D.R., Liem R.K.H.;
"Complete amino acid sequence and in vitro expression of rat NF-M,
the middle molecular weight neurofilament protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-007-1989 (Rel. 12, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament protein)
(Neurofilament medium polypeptide) (NF-M)
                 143;
               Mismatches 167; Indels
                                                                                                                   TSFFTWFMVIALLGVWTSVAVVWFDLVDYEEV----LGKLG-----
                                                                                 8 NASTITIVIDSKNGSVPKSPGKVLKRTVTEDIVTIFSSPAA---
Pred. No. 0.049;
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Xu Z.-S., Liu W.-S., Willard M.B.;
                                                   6 NAKSSGNSSSSGSGSGSTSAGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92332596; PubMed=1321159;
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                   86;
 19.2%;
                 94; Conservative
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   Best Local Similarity
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                                                                                                                                                                           FUNCTION: Neurofilaments usually contain three intermediate filament proteins: L, M, and H which are involved in the maintenance of neuronal caliber.

PTM: There are a number of repeats of the tripeptide K-S-P, NFM is phosphorylated on a number of the serines in this motif. It is thought that phosphorylation of NFM results in the formation of interfilament cross bridges that are important in the maintenance
                                                                                                                                                                                                                                                                                                PTM: Phosphorylation seems to play a major role in the functioning of the larger neurofilament polypeptides (NF-M and NF-H), the levels of phosphorylation being altered developmentally and coincident with a change in the neurofilament function. SIMILARITY: Belongs to the intermediate filament family.
                                                                                                                     "Glycosylation of mammalian neurofilaments. Localization of multiple
                                                                       MEDLINE=93346421; PubMed=8344946;
Bong D.L.-Y., Xu Z.-S., Chevrier M.R., Cotter R.J., Cleveland D.W.,
Hart G.W.,
                                                                                                                                   O-linked N-acetylglucosamine moleties on neurofilament polypeptides
"Identification of six phosphorylation sites in the COOH-terminal tail region of the rat neurofilament protein M.";
J. Biol. Chem. 267:4467-4471(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlycoSuiteDB; P12839; -.
InterPro; IPR006821; Filament_head.
InterPro; IPR001664; Filament_head.
InterPro; IPR001957; Keratin_1.
Pfam; PF00038; filament; 1.
Pfam; PF04732; filament head; 1.
PRINTS; PR01248; TYPE1KERATIN.
Intermediate filament; Coiled coil; Neurone; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION.
MISSING (IN REF. 2).
R -> P (IN REF. 2).
V -> L (IN REF. 2).
MISSING (IN REF. 1).
N; 316C41655B11197D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION
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LINKER 12.
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LINKER 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTIG=CAR
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LINKER 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O-LINKED
                                                                                                                                                               . Chem. 268:16679-16687(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COIL 2B.
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506
506
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608
5 666
17
21
204
95660 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M18628; AAA41696.1; -.
EMBL; Z12152; CAA78136.1; -.
                                                         CARBOHYDRATE-LINKAGE SITES
                                                                                                                                                                                                                                                                                    axonal caliber.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A45669; A45669.
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845 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein.
INIT MET
DOMAIN
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CONFLICT
SEQUENCE
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CONFLICT
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MOD_RES
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                                                             15;
                                                                                                            81 EEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPAVPPEEAEPHTEPEEQVPVEAEP 140
                                                                                                                                                                                                                                                                                                                                                                                                                       640 KESPKEEKVEKKEEKPKDVPDKKKAESPVKEKAVEEMITITKSVKVSLEKDTKEEKPQQQ 699
                                                                                                                                                                                                      141 QNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLE 200
                                                                                                                                                                                                                                                                                                 201 PEVSHEETEHSYHVEETVSODCNODMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVY 260
                                                                                                                                                                                                                                                                                                                                                                                            ----ITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 PET--NRKTDDPEQKAK-----VKKKKPKLLNKFDKTIKAELDAAEKLRK--- 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 ---RGKIEEAVNAFKELVRKYPQSPRAR-----YGKAQCEDDLAEKRRSNEVLRGAI 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              700 EKVKEKAEBEGGSEBEVGDKSPQESKKEDIAINGEVEGKEBEBEQETQEKGSGQEBERGVV 759
                                                                                                                                                                                                                                                                                                                                             -----GEÓEEEGETÉAEGÉGÉEAEAKEEKKTEGKV 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- DISEASE: Involved in acute myeloid leukemias through a chromosomal translocation t(8,16)(pl1,pl3) involving MYST3 and CREBBP.
-!- SIMILARITY: Contains 2 PHD-type zinc fingers.
-!- SIMILARITY: Belongs to the MYST (SAS/NOZ) family.
                                                                                                                                                        453 EEIIEETKVEDEKS----EMEDALTVIAEELAASAK-----EEKEEAEEKEEEPEVEKSP
                                                                                                                                                                                                                                                     --EEGEKEEEEEGQ--EREEEEDEGVKSDQAEEGGS--E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=96376968; PubMed=8782817;

Borrow J., Stanton V.P. Jr., Andresen J.M., Becher R., Behm F.G.,
Borrow J., Stanton V.P. Jr., Disteche C., Dube I., Frischauf A.M.,
Horsman D., Mitelman F., Volinia S., Watmore A.E., Housman D.E.,
"The translocation t(8;16)(p11;p13) of acute myeloid leukaemia fuses
a putative acetyltransferase to the CREB-binding protein.";
Nat. Genet. 14:33-41(1996).

-i- FUNCTION: May represent a chromatin-associated acetyltransferase.
-i- SUBCELLULAR LOCATION: Nuclear.
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MXST histone acetyltransferase 3 (Runt-related transcription factor binding protein 2) (Monocytic leukemia zinc finger protein) (Zinc finger protein 220).
MXST3 OR RUNXBP2 OR ZNF220 OR MOZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                             59; Mismatches 137; Indels 101;
                   Length 845;
            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
4.4%; Score 176.5; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             403 ETYQEVASLPDVPADLLKLSLKRRSDR 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         760 TNGLDVS----PAE----EKKGEDR 776
                                                                                                                                                                                                                                                                                                                                                                                          261 EEQAVYEPLENEGIE----
                                                               90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                     504 VK-SPEAKEE-
                                                                                                                                                                                                                                                                                                                                         546 KEGSSEKDE-
              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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10-OCT-2003
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                                                               Matches
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                  Germonline; 143097; -.
SGD; S0005035; YNL091W.
GO; GO:0009651; P:salinity response; IMP.
                                                                                                                four new open reading frames.";
Yeast 12:599-608(1996).
-!- SIMILARITY: TO S.POMBE SPAC29E6.10C.
                                                                                                                                                                                                                                                                                                                                  POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                   EMBL; X85811; CAAS9826.1; -.
EMBL; Z71367; CAA95967.1; -.
PIR; S52734; S52734.
                                                                                                                                                                                                                                                                                                                                                                                       Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 517 SGD---PGTDD 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        843 VHDLLLPSTNN 853
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                                                                                                                                                                                                                                                                                                                                  761
                                                                                                                                                                                                                                                                                                                      Hypothetical protein
DOMAIN 756 78
                                              SECUENCE FROM N.A.
                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YHUG YEAST
ID YHUG YEAST
AC P38845;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1366 KEETELDS-EEEQPSHDTSVVSEQMA------GSEDDHEEDSHTKEELIEL 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1410 KEE-EEIPHSELDL-----ETVQAVQSLTQEESSEHEGAY--QDCEETLA---- 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 EDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 INKFDKTIKAELDAAEKLRKRGKIEEAVNAFKELVRKYPQSPRARYGKAQCEDDLAEKRR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                 122 EEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 VVEDERLHHDTDD-----VTYQVYEEQAVYEPLENE-GI-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 -EITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPETNRKTDDPEQKAKVKKKKPKL
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                              MET-RICH.
BREAKPOINT FOR TRANSLOCATION TO FORM
                                                                                                                                              Proto-oncogene; Chromosomal translocation; Zinc-finger; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                              88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Hypothetical 141.5 kDa protein in YPT53-RHO2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                      4.4%; Score 175; DB 1; Length 2004; 22.7%; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                            48; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                               225054 MW; 9FFBBAC3792854BA CRC64;
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                                                                                                                                                                                                                                                                                                        POLY-SER.
GLN/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
                             GO; GO: 0006323; P:DNA packaging; TAS. InterPro; IPR005818; Histone H1/H5. InterPro; IPR00217; MOZ SAS. InterPro; IPR001965; Znf PHD. Pfam; PF01853; MOZ SAS, I. Pfam; PF01628; PHD; 2. SMART; SM00526; H15; 1. SMART; SM00249; PHD; 2. PROSITE; PS01399; ZF PHD 1; 1. PROSITE; PS50016; ZF PHD 2; 2.
                                                                                                                                                                                                     C2HC-TYPE.
                                                                                                                                                                                                                          POLY-GLU.
POLY-ARG.
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POLY-LYS.
GLU-RICH.
GLU-RICH.
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                                                                                                                                                                                                                                                                                              POLY-GLU
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EMBL; U47742; AAC50662.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                           73; Conservative
          Genew; HGNC:13013; MYST3
MIM; 601408; -.
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1704
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                                                                                                                                                        Nuclear protein.
ZN FING 206
ZN FING 259
DOWAIN 371
ZN FING 538
DOWAIN 788
                                                                                                                                                                                                                                                                                 1267
1411
1593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         460 BDEDEEDYDD-----XSEYAEDSEEVSEYEGIEAVEKPEHDE----KSNGIRETLHLS 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 EDEAKEQIQSLLHEMVHAEHVE-GEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             568 EEEDENEGDDEED-TYDSGLDETDRLEEGRKLIQIAITKLLQSRIMASYHEKQADNNRLK 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 DAAEKLRK---RGKIEEAVNAFKELVRKYPQSPRARYGKAQCEDDLAEKRR--SNEVLRG 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 VSHE----ETEHSYHVEETVSQDCNQDMEEMMSEQENP-----DSSEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 VVEDERLHHDTDDVTYQ--VYBEQAVYEPLENEGIEITE-----VTAPPEDNPVEDSQV-
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STRAIN=S288c / FY1679;
MEDLINE=96367601; PubMed=8771715;
Garcia-Cantalejo J.M., Boskovic J., Jimenez A.;
Sequence analysis of a 14.2 kb fragment of Saccharomyces cerevisiae
"Sequence analysis of a 14.2 kb fragment of Saccharomyces and chromosome XIV that includes the ypt53, tRNALeu and gsr m2 genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 23.3%; Pred. No. 0.19; no es 103; Conservative 66; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1240 AA; 141513 MW; 3FE9D265822D5778 CRC64;
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21;

us-09-903-216-2.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 INERLINKKEEVPEPVAGPIVESSVTEKSPALPQADDPIVETKEVAHNVQELTPQV---EA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 LIHEMVHAEHVEGEDLOQEDGPIGEP-----QQEDDEFLMATDVDDRFETLEPEVSHE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 VYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVS-IFPVEEQQEVPPETNRKTDDPEQK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 DLVETQEVAGASRIPEAGG------LLCGKPPRSAGPPSTSNRKKNKRNNKKRRSK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 ETEHSYHVEETVSQDCNQDMEEMMSEQEN--PDSSEPVVEDERLHHDTDDVTYQVYEEQA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 AKVKKKKPKLLNKFDKTIKAELDAAEKLRKRGKIEEAVNAFKELVRKYPQSP----RAR 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 -----SKLVEKREST-EGVLDGSKKVENKAKKDEEVFTLDPIVNKAPKKPLTDEQTAE 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- EOVPVEAEPONIEDEAKEOIOS
                                                                                                                                                                                                                                             STRAIN=S288C / AB972;
MEDLINE=94378003; PubMed=8091229;
MEDLINE=94378003; PubMed=8091229;
Johnston M., Andrews S., Erinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Mohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 LKKKSTKNNKKSNESLDDNEEEDGVTGTTTEDVTGTSREETPL-AEPTNVSKEAPGNFHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----QSADTTQSNGIIGGPGPVLVPNPGEIKEFTEIRDVDAR-----E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                       Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52; Mismatches 132; Indels 124;
01.FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical 51.1 kDa protein in DCD1-MRPL6 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 V-TPLINE-----PEPLPTPEAQISIPESSKVEPVEGSLQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.3%; Score 172; DB 1; Length 465; 22.6%; Pred. No. 0.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 465 AA; 51115 MW; 30880758F37991C7 CRC64;
                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387 GRKSPAVSEEKEKKKKQE--KGSKEVKRSETSKEKKPS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    379 YGKAQCEDDLAEKRRSNEVLRGAIETYQEVASLPDVPA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 DLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 LKERSTSEPAVPPERAEPHTEPE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005634; C:nucleus; IC.
GO; GO:0003677; F:DNA binding; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 265:2077-2082(1994).
-!- SIMILARITY: TO YEAST YNL173C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U10397; AAB68982.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                 NCBI_TaxID=4932;
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                                                                                          YHR146W
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 HGLSD--IVHGLLELEGALVGSSPTEEEVEGTEEVEGTEEEVEGTEEEVEGT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: |: ::::|| |: ::::| | |: :: : |: ::| | 457 LDEBEDELQENDSEFFRVKPIIPRHRWIF 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 EDEEVEGTEEEVEGTEEEVEGTEEEVEGTEEEVEGTEEBVEGTE-DEEVEGTEEEVEGTE 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 EEVEGTEEEVEGTEEEVEGTEEEVEGTEEEVEGTEEEVEGTEKDSSOFDNDRVTLLLRPK 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 TSFFTWF-----MVIALLGVWTSVAVVWFDLV----DYEEVLGKLGIYDADGDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 SSLYKWYFELGTSMKKLTILLYLLTCSAGSIAQDLLSPPGPDEQNLITSYGLVENDSDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 FDVDDAKVLLGLKERSTSEPAVPPERAEPHTEPEEQVPVRAEPQNIEDE---AKEQIQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 LHEMVHA--EHVEG----EDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEV--SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----YQVYE----EQAVYEP---LENEGIBIT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRNPLDIORLIYOHOKYESELEEDDDDDEDVFAPOKMLEDLFSELVWSPRIWHPWDFLLD
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                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Myrtales; Onagraceae; Oenothera.
                                                                                                                                                                                                                                                                                                     MEDLINE=93169690; PubMed=8435856; Nimeyk R., Shoendorff T., Hachtel W.; Mimeyk R., Shoendorff T., Hachtel W.; In-frame length mutations associated with short tandem repeats are located in unassigned open reading frames of Oenothera chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 168; Indels 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.3%; Score 172; DB 1; Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  630 AA; 72781 MW; GAEFFF7DC75B0BAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 TDDPEQKAKVKKKRPK----LLNKFDKTIKAELDAAEKL----
                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-GCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein ycf2 (ORF 2280) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 -EVTAPPEDNPVEDSQV----IVEEVSIFPVEE---
  630 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: Belongs to the ycf2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chloroplast; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82;
                                                                                                                                                                                                                                                                                                                                                                                                           Genet. 23:265-270(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X64615; CAA45896.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 107; Conservative
STANDARD;
                                                                                                                                           Oenothera villaricae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S29796; S29796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           NCBI_TaxID=3941;
                                                                                                                                                                Chloroplast
YCF2 OENVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                     P31569
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---- 387
                                     517 ŘKKKDVFEVLSYPEEATEISKELLRLLNPKTKŘDAPKRPŘQŘWWTKKKQŮKHYELLLDRQ 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note=No experimental confirmation available;
PUTH: B-TYPE LAMINS UNDERGO A SERIES OF MODIFICATIONS, SUCH AS PARNESYLATION AND PROSPHORYLATION. INCREASED PHOSPHOSYLATION OF THE LAMINS OCCURS BEFORE ENVELOPE DISINTEGRATION AND PROBABLY PLAYS A ROLE IN REGULATION LAMIN ASSOCIATIONS.
MISCELLANBOUS: The structural integrity of the lamina is strictly controlled by the cell cycle, as seen by the disintegration and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Lamins are components of the nuclear lamina, a fibrous layer on the nucleoplasmic side of the inner nuclear membrane, which is thought to provide a framework for the nuclear envelope and may also interact with chromatin.

SUBCELLULAR LOCATION: Nucleoplasmic side of the inner nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               respectively. SIMILARITY: Belongs to the intermediate filament family. THIS IS B TYPE LAMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91106216; PubMed=2102682; Hoeger T.H., Zatloukal K., Waizenegger I., Krohne G.; Catloukal K., Waizenegger I., Krohne G.; Catloukal X., Maizenegger I., Krohne G.; Catacterization of a second highly conserved B-type lamin present in cells previously thought to contain only a single B-type lamin."; Chromosoma 99:379-390(1990).
                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      formation of the nuclear envelope in prophase and telophase
RKRGKI -----EEAVNAFKELV-----RKYPQSPRARYGKAQCEDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91339548; PubMed=2102440;
Hoeger T.H., Zatloukal K., Waizenegger I., Krohne G.;
Chromosoma 100:67-69(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing, Named isoforms=2;
Name=B2;
                                                                                                                                                                                                                                                                       01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                        577 RWLITKRSLSKSNGFFRSNTPSESYQYLSNL 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P21619-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P48680-1; Sequence=External;
                                                                                --LAEKR---RSNEVLRG--AIETYQEVASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:96796; Lmmb2.
GO; GO:0005638; C:lamin filament; IDA.
InterPro; IPR001864; IF.
InterPro; IPR001322; IF tail_C.
Pfam; PF00038; filament; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X54098; CAA38032.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B48315; B48315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE LAMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane.
                                                                                                                                                                                                                               LAM2 MOUSE
P21619;
                                                                                                                                                                                                                                                                                                                                        Lamin B2.
                                                                                                                                                                                                                                                                       g
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29;
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PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Nuclear protein; Lipoprotein;
Prenylation; Phosphorylation; Alternative splicing.
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1 MAQRKNAKSGNSSSSGSSGSGSTSAGSSSPGARRETKHGGHKNGRKGGLSGTSFFTWFMV 60

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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Aspartyl beta-hydroxylase 6.6 kb transcript (Aspartyl beta-hydroxylase
                                      PEEABPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQ
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2310005F16RIK OR ASPH.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutherra, Rodentia, Sciurognathi, Muridae, Musinae,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F., Friedman P.A.;
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EMBL; AF289487; AAG40809.1; -.
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STRAIN-BALB/C; TISSUE-Liver;
MEDLINE-20564328; PubMed=10956665;
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287 SIISBEINVASVEBQODTPP-------VKKKKPKLLNKPDKTIKAELDAAEKL
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                                                        InterPro; IPR007943; Asp-B-hydro N.
InterPro; IPR007943; Asp-B-hydro N.
InterPro; IPR001440; TPR.
InterPro; IPR001440; TPR.
InterPro; IPR008441; TPR.
Pfam; PF05279; Asp-B-Hydro N; 1.
Pfam; PF05118; Asp Arg Hydrox; 1.
SEQUENCE 739 AA; 82841 MW; 4DF9F642512CA4EB CRC64;
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                                                                                                                                                                                                                                                                                                                    .Match
Local Similarity 80.7%; Pred. No. 2.8e-183; e8 619; Conservative 41; Mismatches 70;
AF289486; AAG40808.1;
                             MGD; MGI:1914186; Asph
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                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Ovary, and Uterus;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
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MGD; MGI:1914186; Asph.
InterPro; IPR007943; Asp-B-hydro_N.
InterPro; IPR0079803; Asp-B-hydrox.
InterPro; IPR001440; TPR.
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Pfam; PF05118; Asp Arg Hydrox; 1.
SMART; SM00028; TPR; 2.
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                             Aspartate-beta-hydroxylase
                                                                                               musculus (Mouse)
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                                                      651 LEKFPETTGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETRT 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317
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574 ERNWKLIRDEGLMVMDKAKGLPLPEDENLREKGDWSQFTLWQQGRKNENACKGAPKTCAL 633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Body;
MEDILINE=22254683; PubMed=12466851;
The PANTOM CONSOrtium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 TSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GSFFTWFWVIALLGVWTSVAVVWFDLVDYEEVLGKLGVYDADGDGDFDVDDAKVLLGLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 SEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVED
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                       711 WEEGKVLIFDDSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI 758
                                                                                                                                                                                                                       694 WEEGKVLIFDDSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81492 MW; F3CE979F8FC9C3D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                01.MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                               725 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1914186; Asph.
InterPro; IPR007943; Asp-B-hydro N.
InterPro; IPR001903; Asp-Brg_Hydrox.
InterPro; IPR001440; TPR.
InterPro; IPR008941; TPR-like.
Pfam; PF05279; Asp-B-Hydro N; 1.
Pfam; PF05118; Asp-B-Hydrox; 1.
SMART; SM00028; TPR; 2.
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                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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Aspartly beta-hydroxylase. ASPH.
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                                                  557
                                                                                                                                                                                                        617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AR035735; BAC29171.1; -.
                                     LPDVPADLLKLSLKRRSDRQQFLGHMRGSLLTLQRLVQLFPNDTSLKNDLGVGYLLIGDN
                                                                                   471 DNAKKVYEEVLSVTPNDGFAKVHYGFILKAQNKIAESIPYLKEGIESGDPGTDDGRFYFH
                                                                                                                                              ERNWKLIRDEGLAVMDKAKGLFLPEDENLREKGDWSQFTLWQQGRRNENACKGAPKTCTL
                                                                                                                                                                                               558 ERNWKLIRDEGLMVMDKAKGLFLPEDENLREKGDWSQFTLWQQGRKNENACKGAPKTCAL
                                                                                                                                                                                                                            LEKFPETTGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETRT
                                                                                                                                                                                                                                                618 LEKFSETTGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKBGCKIRCANBTRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
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                                                                                                                                 531 LGDAMQRVGNKEAYKWYELGHKRGHFASVWQRSLYNVNGLKAQPWWTPKETGYTELVKSL
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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80.7%; Pred. No. 7.3e-168;
ive 38; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/6J; TISSUE=Urinary bladder;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                    Created)
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InterPro; IPR007943; Asp-B-hydro_N.
InterPro; IPR007943; Asp-B-hydro_N.
InterPro; IPR008940; Prenyl_trans.
InterPro; IPR001440; TPR.
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Pfam; PF05118; Asp Arg Hydrox; 1.
SMART; SM00028; TPR; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Aspartate-beta-hydroxylase.
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Matches 566; Conservative
                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 EEVLNVTPNDGFAKVHYGFILKAQNKISESIPYLKEGIESGDPGTDDGRFYFHLGDAMQR 437
                                                                                                                                        238 SSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEE 297
                                                                                                                                                                                                                                                                                                                                                   257
                                                                                                                                                                                                                                                                                                                                                                                                                         417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               538 VGNKEAYKWYELGHKRGHFASVWQRSLYNVNGLKAQPWWTPKETGYTELVKSLERNWKLI 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   658 TGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETRIWEEGKVL 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 EEVLSVTPNDGFAKVHYGFILKAQNKIAESIPYLKEGIESGDPGTDDGRFYFHLGDAMQR
                                                                                                                                                                                                                                                                                                                                                                                                                         358 EEAVNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVASLPDVPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       598 RDEGLAVMDKAKGLFLPEDENIREKGDWSQFTLWQQGRRNENACKGAPKTCTLLEKFPET
                                                                                                                                                                                    298 VSIFPVBEQQEVPPETNRKTDDPEQKAKVKKKKPKLLNKFDKTIKAELDAABKLRKRGKI
                                                                                                                                                                                                                                                                                                                                                   212 INVASVEEQODTPP-----VKKKKPKLLNKFDKTIKAELDAAEKLRKRGKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 VGNKEAYKWYELGHKRGHFASVWQRSLYNVNGLKAQPWWTPRETGYTELVKSLERNWKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 RDEGLMVMDKAKGLFLPEDENLREKGDWSQFTLWQQGRKNENACKGAPKTCALLEKFSET
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Henderson N.L., Dinchuk J.E., Burn T.C., Hollis G.F., Friedman P.A.;
Henderson N.L., Dinchuk J.E., Burn T.C., Hollis G.F., Friedman P.A.;
Benderson (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF289215; AAG39913.1; --
EMBL, AF289206; AAG39913.1; JOINED.
EMBL, AF289207; AAG39913.1; JOINED.
EMBL, AF289207; AAG39913.1; JOINED.
EMBL, AF289208; AAG39913.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=20564328; PubMed=10956665;
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                                                                                                                                                                                                                                                   72.6%; Score 2919.5; DB 11; Length 689; 74.7%; Pred. No. 5.2e-166; cive 39; Mismatches 68; Indels 87;
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                                                                                                                                                                InterPro, IPR008941; TPR-like.
Pfam. PF05279; Asp-B-Hydro N; 1.
Pfam; PF05118; Asp-B-Hydrox; 1.
SEQUENCE 689 AA; 77319 MW; 9C8916DF109F432C CRC64;
                                                                                                 MGD; MGI:1914186; Asph.
InterPro; IPR007943; Asp-B-hydro N.
InterPro; IPR007943; Asp_Arg_Hydrox
InterPro; IPR001440; TPR.
EMBL; AF289209; AAG39913.1; JOINED.
EMBL; AF289210; AAG39913.1; JOINED.
EMBL; AF289211; AAG39913.1; JOINED.
EMBL; AF289212; AAG39913.1; JOINED.
EMBL; AF289212; AAG39913.1; JOINED.
EMBL; AF289213; AAG39913.1; JOINED.
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Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved isoform of asph missing the catalytic domain share exons with
                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=20564329; PubMed=11007777;
Treves S., Periotto G., Moccagatta L., Gambari R., Zorzato F.;
"Molecular Cloning, Expression, Functional Characterization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.7%; Score 1636; DB 4; Length 313; 99.7%; Pred. No. 7.3e-90; arive 1; Mismatches 0; Indels (
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EMBL; AF289489; AAG40811.1; -.

InterPro; IPROD1943; AAP-B-N-MATO_N.

Pfam; PF05279; ASp-B-Hydro_N; 1.

SEQUENCE 313 AA; 34646 MW; 7885A18B81CD6D0D CRC64;
                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Aspartyl beta hydroxylase 2.8 kb transcript.
Homo sapiens (Human).
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Matches 312; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQ 244
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                                                                                                                                                                                                                                                                                                                                              5 KETKHGGHKNGRKGGLSGTSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLAKAKDFRYN
                                                                                                                                                                                                                                                                                                                                                                                        85 -----GKLGIYDADGDGDFDVDDAKVLLGLKERSISEPAVPPEEAEPHTEPEEQVPVEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 VYEBQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPDT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Chromosomal Localization, and Gene Structure of Junctate, a Novel Integral Calcium Binding Protein of Sarco(endo)plasmic Reticulum Membrane.";
                                                                                                                                                                                                                                                                   15;
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                                                                                                                                                                                                                         36.2%; Score 1457.5; DB 4; Length 299; 94.2%; Pred. No. 3.1e-79; ive 2; Mismatches 0; Indels 15;
                                                                                                                                                                                                                                                                                                         34 RETKHGGHKNGRKGGLSGTSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVL--
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85.9%; Pred. No. 1.8e-74;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC025236; AAH25236.1; -.
InterPro; IPR007943; Asp-B-hydro_N.
Pfam: PF05279; Asp-B-Hydro_N; 1.
SEQUENCE 270 AA; 29757 Mw; 8551773C7272202A CRC64;
                                                              J. Biol. Chem. 275:39555-39568 (2000).

EMBL, AR366765, AAG42257.1;

GO, GO:000599; C:endoplasmic reticulum membrane; NAS.

GO, GO:0005509; F:calcium ion binding; NAS.

InterPro; IPR007943; Asp-B-hydro_N.

Pfam; PF05279; Asp-B-hydro_N.

FROWNER 299 AA; 33815 NW; 658F88C34ECCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 PEEAEPHTEPEEQVPVEAEPQNIEDEAKEGIQSLLHEMVHAEH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 AA.
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Best Local Similarity
Matches 278; Conserva
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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RAMEDINE-20186006; PubMed=10731132;

RAMEDINE-20186006; PubMed=10731132;

RA Adams M.D. Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holf R.A., Forderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Worthman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Benne P.V., Berman B.P., Bhandrain D., Botchan M.R., Bouck J., Brokstein P., Borchard S.,

RA Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Borthos B., Delcher A., Deng Z., Mays A.D., Daviss P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Posler C., Gabrielian A.E., Gang C., Ferraz C., Ferriars S., Pleischmann W.,

RA Harris N.L., Harrey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Howland T.J., Weil M.-H., Ibegwam C.,

RA Jalai M., Ralush F., Karpen G.H., Re Z., Kennison D.,

RA Jalai M., Ralush F., Karpen G.H., Re Z., Kennison D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Razzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Rainer R., Sanders R.D., Sanders R.D., Scheeler F., Shen H.,

RA Spier B., Spradling A.C., Stapleton M., Strong R., Wang X.,

RA Shire B.C., Siden-Kiamos I., Sinneson D.R., Rang R., Tector C., Turner R., Venter E., Wang A.H., Wang S., Fan Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang S., Fan Svirskas R., Tector C., Turner R., Venter E., Spradling A.C., Stapleton M., Strong R., Wang R., Reise R., Tector C., Turner R., Venter E., Spradling A.C., Stapleton M., Strong R., Wang R., Tector C., Turner R., Venter E., Spradling A.C., Stapleton M., Strong R., Nelson D.E., Tector C., Turner R., Venter E., Stapleton R., Reise R., Strong R., 
181 QEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSE 240
                                                                                              241 PVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSI 300
                                                                                                                                         198 PVVEDERLHHDTDDVTYQVYEEQAVXEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSI 257
                                            ----ETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20564328; PubMed=10956665;
Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Aspartyl beta -Hydroxylase (Asph) and an Evolutionarily Conserved
Isoform of Asph Missing the Catalytic Domain Share Exons with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
1-CT-2003 (TrEMBLrel. 25, Last annotation update)
Aspartyl beta-hydroxylase variant 1 (CG8421-PA)
ASPH OR CG8421 OR CG18658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 275:39543-39554 (2000).
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MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                   301 FPVEEQQEVPPET 313
                                                                                                                                                                                                                                                     258 PPVEBOÓBVPPDT 270
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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"Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved isoform of asph missing the catalytic domain share exons with
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EMBL; AF289488; AAG40810.1; -.
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MEDLINE=20564328; PubMed=10956665;
Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Lin
O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI 758
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(TrEMBLrel. 16, Last seq.
(TrEMBLrel. 24, Last anno
152 QSLLHEMVHAEHVEGEDLQQEDG-
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Q93178; Q93876;
01-FEB-1997 (TrEMBLrel. 02, C
01-NOV-1998 (TrEMBLrel. 08, L
01-OCT-2003 (TrEMBLrel. 25, L
K09A9.6 protein.
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                                                                                                        235 EQEN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 TSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKE 111
                                                                                                                                                                                                                                                        52 TSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKE 111
                                                                                                                                                                                                                                                                                                                                                           112 RSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQ 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 EDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMS 231
                                                                                                                                                                                           1 MAPRKNAKGGGGNSSSSGSGSGSGSGSPSTGSSGSSSSPGARREAKHGGHKNGRRGGISG 60
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                                                                                                                                                     1 MAORKNAK-SSGNSSSSGSGSGS-----TSAGSSSPGARRETKHGGHKNGRKGGLSG
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                24.8%; Score 998.5; DB 11; Length 308; 64.3%; Pred. No. 8e-52; Live 30; Mismatches 62; Indels 23;
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Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015281; A4H15281.1; -
MGD; MGT:1914186; Asph.
InterPro; IPR007943; Asp-B-hydro_N.
Pfan; PF05279; Asp-B-Hydro_N; 1.
SEQUENCE 292 AA; 31568 MW; B3A470A46EC24B6D CRC64;
  33142 MW; F208C2C31C595282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                  Local Similarity 64.3
les 207; Conservative
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308 AA;
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175 ADGLAGEPQPEVEDFLTVTDSDDRFEDLEPGTVHEEIEDTYHVEDTASQNHPNDMEEMTN 234
                                                         232 EQENPOSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDS 291
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                                                                                                                ---SEEVRHODYDE-PVYEPSEHEGVEIS-----DNTIDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 RETKHGGHKNGRKGGLSGTSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 LLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYH
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.1%; Score 890; DB 11; Length 270; 63.9%; Pred. No. 2e-45; ive 30; Mismatches 57; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hong C.-S., Kim D.H., "Cloning of mouse junctin homologs.";
"Cloning of mouse junctin homologs.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF302653, AAL09319.2; -.
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MGD; MGI:1914186; Asph.

InterPro; IPR007943; Asp-B-hydro N.

Pfam; PF05279; Asp-B-Hydro N; 1.

SEQUENCE 270 AA; 29949 MW; 70BB13DC01B51701 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                292 QVIVEEVSIFPVEEQQEVPPET 313
                                                                                                                                                                                                                       PRT;
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89 IYDADGDGDFDVDDAKVLLGLKERSTSEPAVPPEBAEPHTEPEBQ------VPVEAEPQ 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 NIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDG-----PTGEPQQEDDEFLMATDVDDR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 FETL-----EPEVSHEETE--HSYHVEET------VSODC-NODMEE- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 RKSLLVTKKKTKSMVERILDDEFDDEDDDD------BDDDSEVNK----N 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNPVEDSQVIVEEVSIFPVEEQGEVPPETNRKTDDPEQKAKVKKKKPKLLNKFDKTIKAE 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             635 DPKFYYQLGHGLTTLGRKSEADAVYQKAAQMGVFMTAQQRSLYNIEGLTGRAWWAMDQTP 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416 DREDDDBDDVDERIS---------DRDSSSSYKRHAITTKEEIGFRDI 454
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                                                                                                                                                                                                                                                                                                                                                                                    Wilson R., Annscound R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Ropra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
19.8%; Score 798; DB 5; Length 872;
Best Local Similarity 26.8%; Pred. No. 3.1e-39;
Matches 191; Conservative 144; Mismatches 278; Indels 100; Gaps
                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases
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SEQUENCE 872 AA; 99456 MW; 8CA3E03489A9848B CRC64;
Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro, IPR007803; Asp Arg Hydrox.
InterPro, IPR008940; Prenyl_trans.
InterPro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, Z79561, CAB01887.1; -.
EMBL, Z79556; CAB01887.1; JOINED.
EMBL, Z79596; CAB01859.1; -.
EMBL, Z79601; CAB01859.1; JOINED.
PIR; T18861; T18861.
WormPep; K09A9.6; CE11982.
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                                                   Submitted (AUG-1996)
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                SEQUENCE FROM N.A
                                             NCBI_TaxID=6239;
                                                                                                                                                                                   Swinburne
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583 YTELVKSLERNWKLIRDEGLAVMDKAKGLFLPEDENLREKGDWSQFTLWQQGRRNENACK 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 GDGDFDVDDAKVLLEGPGGLAKRKTKAKGLKERSPSERTFPP-EAETHAELEEQAP---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 PQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 EPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---EGADL-EADGLAGEPOPEVEDFLTVTDSDDRFEDL 153
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                   34 RETXHGGHKNGRKGGLSGTSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDAD
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                                                                      543 GAPKTCTLLEKFPETTGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKI
                                                                                              53; Gaps
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                                                                                                                                                 703 RCANETRIWEEGKVLIFDDSFEHEVWQD---ASSFRLIFIVDVWHPELTPQQR 752
                                                                                                                                                                    814 RVGNETKGWRSGKFIIYDDSFEHELQFDGASSSSFRLVLTIQLWHPEVQPHQR 866
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Acodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 YDE-PVYEPSEHEGVEIS------DNTIDDSSIISBEINVASVEEQQDTPPDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hong C.-S., Kim D.H.;
"Cloning of mouse junctin homologs.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1914186; Asph.
InterPro; IPR007943; Asp-B-hydro_N.
Pfam; PF05279; Asp-B-Hydro_N; 1.
SEQUENCE 259 AA; 28455 MW; A6740C6CF199E093 CRC64;
                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19) Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Cardiac junctare 2.
ASPH OR 3110001L23RIK.
                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 55.4*
Matches 163; Conservative
                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

May 5, 2004, 11:01:09; Search time 23 Seconds Run on:

(without alignments)
1701.412 Million cell updates/sec

US-09-903-216-2

4022 1 MAQRKNAKSSGNSSSSGSGS.....IVDVWHPELTEQQRRSLPAI 758 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

389414 segs, 51625971 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADIES

		dif			SUMMARIES		
Result No.	Score	Query	Query Match Length	DB	ID	Description	
1	1334	33.	255	<u>ا</u> ه	40-485-	Sequence 2, Appli	
63	1320	32.	255	4	-09-702-705-180	യ	
Э	1320	32.	255	4	-457-18	Sequence 1806, Ap	
4	1320		255	4	09-671-325-180	Sequence 1806, Ap	
2	199	4.	783	9	31168-	Patent No. 5231168	
9	O)	4	320	4	'n	S	
7	Ø.	4.	1018	Н	-08-072-6	Sequence 2, Appli	
80	O)	4	1018	7	-08-719-	Sequence 2, Appli	
σ	σ	4	1018	m	-09-092-	Sequence 2, Appli	
10	σ	4	1162	7	-08-728-	Sequence 2, Appli	
11	σ	4.7	1162	4	-298-568-	Sequence 2, Appli	
12	190.5	4.7	1162	4	US-09-410-399-2	Sequence 2, Appli	
13	ထ	4.7	312	4	-09-328-352-	Sequence 8015, Ap	
14	177.5	4.4		٣	-08-961-083-21	218,	
15	r	7		4	US-09-536-784-218		
16	177	4	327	4	-09-489-	10158	
17	172.5	4.3	700	4	-09-107-5	5094,	
18	9	4.1	411	7	US-08-741-134-6	6, Apr	
19		4.1	2662	4	9-265-60-	31,	
20	٠	4.0	310	4	-09-252-9	2651	
21	162	4.0	1282	4	9	541	
22	9	4.0	688	m	US-09-141-047-8	ω,	
23	56.	•	206	a	-1	equence 19,	
24	•	3.9	206	m	5-699-1	19,	
25	56.		206	m	US-09-273-565-19	equence 19,	
56	56.	•	206	4	7	19,	
27	2		206	4	US-09-661-468-19	equence 1	

Sequence 19, Appl	Sequence 3944, Ap	Sequence 94, Appl	Sequence 94, Appl		7	Sequence 2, Appli	Sequence 4, Appli	Sequence 3, Appli	7	11,	32,	Sequence 10, Appl	Sequence 21, Appl	Sequence 6, Appli	Sequence 6, Appli	90,	Sequence 90, Appl
US-09-976-165-19	US-09-107-532A-3944	US-08-056-200-94	US-08-800-644-94	US-08-242-932-2	US-08-714-481-2	PCT-US95-06111-2	US-08-875-435B-4	US-09-554-080A-3	US-09-554-080A-2	US-09-914-259-11	US-09-216-393B-327	US-08-923-992A-10	US-09-914-259-21	US-08-533-306A-6	US-08-742-923A-6	US-08-961-083-90	US-09-536-784-90
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206	1196	1898	1898	984	984	984	1972	404	436	3878	571	1164	196	816	816	258	258
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156.5	154.5	153.5	153.5	152.5	152.5	152.5	151.5	151	151	150.5	150	149.5	149	148.5	148,5	148	148
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ALIGNMENTS

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59 MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA 118
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                                                           GENERAL INFORMATION:
APPLICANT: RAGOSEVICH, James A.
TITLE OF INVENTION: A GENE ENCODING A NOVEL MARKER FOR TITLE OF INVENTION: CANCER NUMBER OF SEQUENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: ADDRESS: ADDRESSE: BRINKS, HOFER, GILSON & LIONE
                                                                                                                                                                                                                  ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Plaza Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/09/040,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/040,485
FILING DATE: 17-MAR-1998
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice 0.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 8998/3
TELECHMONIALCATTON INFORMATION:
TELECHMONIALCATTON INFORMATION:
TELECHMONIALCATTON INFORMATION:
TELECHMONIALCATTON INFORMATION:
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TELECHMONIALCATTON INFORMATION:
                    Sequence 2, Application US/09040485 Patent No. 6166176
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 255 amino acids
amino acid
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Matches 254; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-040-485-2
                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinoi
US-09-040-485-2
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119 VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE 178

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61 VPPERARPHTEPERGVPVBAEPQNIEDBAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE 120
                                                                                                                                                                                             239 SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEV 298
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                                                                                   POQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS
                                                                                                                                    121 PQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Tom
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Pan, Liqun
APPLICANT: Pan, Liqun
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCE;
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1806, Application US/09702705 Patent No. 6504010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
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US-09-702-705-1806
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US-09-702-705-1806
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LENGTH: 255
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                        299
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; Sequence 1806, Application US/09736457 ; Patent No. 6509448 ;; GENERAL INFORMATION:

US-09-736-457-1806

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178
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GENEKAL ...

APPLICANT: Wangy, ACLES APPLICANT: Dodes, Michael A.

APPLICANT: Lodes, Michael A.

APPLICANT: Fanger, Gary

APPLICANT: Vedvick, Tom

APPLICANT: Vedvick, Tom

APPLICANT: Retter, Marc

APPLICANT: Marc

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APPLICANT: Marc

APPLICANT: Darrick

APPLICANT: Darrick

APPLICANT: Darrick

TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER

FILE REFERENCE: 210.14.78C12

CURRENT APPLICATION NUMBER: US/09/671,325

CURRENT APPLICATION NUMBER: US/09/671,325

CURRENT APPLICATION NUMBER: US/09/671,325

CURRENT APPLICATION NUMBER: Darrick

NUMBER OF SEQ ID NOS: 1825

COFTWARE FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 POOEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSODCNODMEEMMSEQENPDS
                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210.21.4.79C15
CURRENT APPLICATION NUMBER: US/09/736,457
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FRAESEQ FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.8%; Score 1320; DB 4; Length 255; 98.8%; Pred. No. 2.1e-99; live 1; Mismatches 2; Indels
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Patent No. 6667154
GENERAL INFORMATION:
     Bangur, Chaitanya S.
Lodes, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 SIFPVEEQQEVPPET 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 SIFPVEEQQEVPPDT 255
                                                     Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
Fan, Ligun
Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252; Conservative
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Matches 252; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 KVDVQPKIVDLQIIEPNFVDSQPNPQEPVEFSFVKIEKVPSEENKHA.SVDPEVKE--KE 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VEEQQEVPPETNRK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 YPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVASLPDVPAD------LLKLS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 SELHENEVAHPEIVEIEEV--FPEPNQNNEFQEINEDDKSAHIQHEIVEVEEILPEDDKN 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 TDDPEQKAKVKKKPKLLNKFDKTIKABLDAAE-----KLRKRGKIEBAVNAFKELVRK 370
                                                                                                                                           9
                                                                                                                                                                                                                                                   179 PQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS
                                                                                                                                                                                                                                                                                                                                                  181 SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTVPPEDNPVEDSQVIVEEV
                                                                                                                                         1 MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
                                                                                                                                                                               119 VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE
                                                                                                                                                                                                                                                                          121 PQQEDDBFLMATDVDDRFETLELEVSHEETEHSYHVBETVSQDCNQDMEEMMGEQENPDS
                                                                                                                                                                                                                                                                                                                           SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 SVSEPAEHVEIVSEKST--SEPAEHVESV----SEQSNNEPSEKKÖGPVPSXPFEEIE
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                                                                                                         59 MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
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4.9%; Score 199; DB 6; Length 783;
Best Local Similarity 20.6%; Pred. No. 1.6e-07;
Matches 143; Conservative 134; Mismatches 237; Indels 180;
                                   Length 255;
                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5231168
APPLICANT: DZIEGIEL, MORTEN; BORRE, MARTIN; JEPSEN, SORI; VOUST, JENS; RIEMEZCK, KLAUS; WIND, ANNETTE; JAKOBSEN, PALLE I) TILE OF INVENTION: MALARIA ANTIGEN NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/409,658
FILING DATE: 18-SEP-1989
                                  32.8%; Score 1320; DB 4; 98.8%; Pred. No. 2.1e-99; iive 1; Mismatches 2;
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                                                 Best Local Similarity 96.0
Matches 252; Conservative
                                Query Match
Best Local Similarity
US-09-671-325-1806
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APPLICATE: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AREQUINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AREQUINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR STILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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423 LKRRSDRQQFLGHMRGSLLTLQRLVQLFPNDTSLKNDLG-----VGYLLIGDNDNAKKV 476
                                                                                                                                                                                        607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         591 ERNWKLIRDEGLAVMDKAKGLFLPEDENLREKG-----DWSQFTL-WQQGRRNENACK 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 643 GAPKICTLLEKFPETTGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIP-KEGCK 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 LCPKTVELVSRIPNVKGA-----MFTLLPGGSHLNPHRDPFGGSLRYHLGLSTPNSDNCR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81
                                                           504 EILPEDKNEKVQH-----EIVEVEEILPED---KNEKGQHEIVEVEEILPEEDKNEKGQ
                                                                                                                          477 YE--EVLSVTPNDGFAKVHYGFI------LKAQNKIAESIPYLKEGIESGDPGTD
                                                                                                                                                              524 DGRFYFHLGDAMQRVGNKEAYKWYELCHKRGHFASVWQRSLYN---VNGLKAQPWWTPK-
                                                                                                                                                                                                                                                                                        580 ---ETGYTELVKSLERNWKLIRD-----EGLAVMDKAKGL--FLPEDENLREKGDWSQFT
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TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,
TITLE OF INVENTION: Monoclonal Antibodies, and Diagnostic Assays
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           630 LW-----QQGRRNENACKGAPKTCTLLEKFPETT 658
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Similarity 25.9%; Pred. No. 5.7e-08;
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/08072610; Patent No. 5532133; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58; Conservative
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LENGTH: 320
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US-08-072-610-2
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Best Local
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895 SDEKWKKWFKAEVKSQIDS---HLKKWMND----THSNLFKILVKD-MSQFENKKTKEWL 946

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27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 HEMVHAEHVEGEDLQQEDGP-TGEPQQED--DEFLMATDVDDRRETLEPEVSHEETEHSY 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                593 ------EGEGEPTEEEPREGEPTEGEVPEEELEATPEDD-FELEEP--TGEEVEETV 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       533 İKDPDAGEAVTVPSKEAPVQVPVAVGPAQEVPTEELMQLQEDDFELEGTAEAPEEGELVL 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           641 BGEETAE---GEEVPEVPAEVE-------EVEEVPAEVEEVPESVEEV 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 GIBITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPETNRKTDDPEQKAKVKKKKPK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 LLNKFDKTIKAELDAAEKLRKRGKIEEAVNAFKELVRKYPOSPRARYGKAQCEDDLAEKR 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 RS-----NEVLRGAIETYQEVASLPDVPADLLKLSLKRRSDRQQFLGHMRGSLLTLQRL 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         447 VQLFPNDTSL------KNDLGVGYLLIGDNDNAKKVYEEVLSVTPND--GFAKVHY 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495 G-----FILKAQNKIAESIPYLKEGIESGDPGTDDGRFYFHLGDAMQRVGNKEAYKWY 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.9%; Score 197.5; DB 1; Length 1018;
23.2%; Pred. No. 3.1e-07;
tive 86; Mismatches 205; Indels 133; Gaps
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,610
FILING DATE: 19930602
                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: GOGOTIS, Adda
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/07686
TELECOMMUNICATION INFORMATION:
TELEFRONE: (212)527-7700
                                                                                                                                               : Floppy disk
IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212/)
TELEFAX: 236687
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1018 amino acids
"VPE: AMINO ACID
"'PE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Plasmodium vivax
IMMEDIATE SOURCE:
CLONE: PVMB3.3.1
                  ADDRESSEE: Darby and Darby STREET: 805 Third Ave. CITY: New York
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Matches 128; Conservative
                                                                                                           ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: YES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            OPERATING SYSTEM:
                                                                              New York
                                                                                                                                                                                                                                                                   FILING DATE: 19
CLASSIFICATION:
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FRAGMENT TYPE: C
ORIGINAL SOURCE:
                                                                                               USA
                                                                                                                                                                       COMPUTER:
                                                                                               COUNTRY:
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947 MNHWKKNERGYGSESFEVMTTSKLLNVAKSREWYRANPNINRERRELMKWFLLKENEYLG 1006
  ----ASVWQRSLYNVNGLKAQ--PWWTPKETGY-- 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 HEMVHAEHVEGEDLQQEDGP-TGEPQQED--DEFLMATDVDDRFETLEPEVSHEETEHSY 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 HVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENE 272
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4.9%; Score 197.5; DB 2; Length 1018;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
Matches 128; Conservative 86; Mismatches 205; Indels 133;
                                                                                                                                                                                                                             Sequence 2, Application US/08719822B
Patent No. 5874527
GENERAL INFORMATION:
APPLICANT: Barnwell, John
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby and Darby
STREET: 805 Third Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/719,822B FILING DATE: 09/30/96
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ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda
REGISTRATION NUMBER: 29,714
548 ----ELGHKRGHF----
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INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 1018 amino acids
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(212)753-6237
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1007 QRMEKANDSLEKS 1018
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                                                                               584 -- TELVKSLERN 593
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CLONE: PVMB3.3.1
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ZIP: 10022-7513
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                                                                                                             393 RS-----NEVLRGAIETYQEVASLPDVPADLLKLSLKRRSDRQQFLGHMRGSLLTLQRL 446
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273 GIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPETNRKTDDPEQKAKVKKKKPK 332
                                                                                                                                                                                                                                                  447 VQLFPNDTSL------KNDLGVGYLLIGDNDNAKKVYEEVLSVTPND--GFAKVHY 494
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APPLICANT: Barnwell, John
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,
TITLE OF INVENTION: MONOclonal Antibodies, and Diagnostic Assays
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby and Darby
STREET: 805 Third Ave.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,458
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REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17686US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/719
FILING DATE: 09/30/96
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STREET: 805 ...
CITY: New York
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                                                                                                                                                                        4.9%; Score 197.5; DB 3; Length 1018;
23.2%; Pred. No. 3.1e-07;
Live 86; Mismatches 205; Indels 133; Gaps
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APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Relamon, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
                                                                                                                                                                                                                                                                   109 LKERSTSEPAVPPEEAEP----HTEPEEQVPVEAEPQNIED----
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Encoding Same And Uses Thereof
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STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08728323A Patent No. 5948676
                FRAGMENT TYPE: C-terminal ORIGINAL SOURCE: ORGANISM: Plasmodium vivax IMMEDIATE SOURCE: CLONE: PWMB3.3.1
                                                                                                                                                                                                                        Conservative
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TITLE OF INVENTION: Sarc
TITLE OF INVENTION: Enc
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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Matches 128; Conserv
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STATE: New York
COUNTRY: U.S.A.
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ANTI-SENSE:
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APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: RAYe, Kenneth M.
ITILE OF INVENTION: RHADING VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADING TITLE OF INVENTION: RHADING VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REPRESENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER PILING DATE: 1998-11-19
SARLIER PEDIA ONS: 3
SOFTWARE: PALENTIN ONS: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
4.7%; Score 190.5; DB 2; Length 1162;
Best Local Similarity 22.9%; Pred. No. 1.4e-06;
Matches 70; Conservative 68; Mismatches 123; Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                              Patentin Release #1.0, Version #1.30
                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
                                                                                          PC-DOS/MS-DOS
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Patent No. 6322792
GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                  NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1162 amino acids
                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                SOFTWARE:
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GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, wurray A.
ITLLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 EEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQ 181
                                                                                                                                                                                                            698 DEQEQQDEQEQQDEQEQQDEQQQDEQQQQ-----DEQQQQDEQQQQD----EQQQ 743
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                                                                       Length 1162;
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                                                             Query Match
4.7%; Score 190.5; DB 4; Length 1
Best Local Similarity 22.9%; Pred. No. 1.4e-06;
Matches 70; Conservative 68; Mismatches 123; Indels
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ORGANISM: Kaposi's sarcoma-associated herpesvirus
ORGANISM: Kaposi's sarcoma-associated herpesvirus
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; Patent No. 6482587
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Best Local Similarity 22.5*
Best Local Similarity 22.5*
T0; Conservative
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LENGTH: 1162
    US-09-410-399-2
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Query Match
4.4%; Score 177.5; DB 3; Length 565;
Best Local Similarity 22.5%; Pred. No. 5.5e-06;
Matches 114; Conservative 71; Mismatches 199; Indels 123;
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ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 ED-----NPVEDSQV---IVEEVSIFPVE---
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                                                                                                      PB340P2
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                                 ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34(
TELEPONE: (301) 309-8504
INFORMATION FOR SEQ ID NO: 218:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 LRKRGKIEEAVNAF-----
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                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
APPLICATION NUMBER:
                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-536-784-218
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APPLICANT: Gary L. Brecon et al.
APPLICANT: Gary L. Brecon et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 RDPYAGSLRYHLGLITPNDDRCFIDVDGERYSWRDGQSVVFDETYIHYAENKTDQNRIIF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 620 REKGDWSQFTLWQQGRRNENACKGAPKTCTLLEKFPETTGCRRGQIKYSIMHPGTHVWPH 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 FFKTGWKRFYLKWYESSHPSAAELCPKTTALLKTLPTIKAA-----MFTELAPDSRLVRH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     680 TGPTNCRLRMHLGLVIPKEG-CKIRCANETRTWEEGKVLIFDDSFEHEVWQDASSFRLIF 738
                        356 KIEBAVNAFKELVRKYPQ----SPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVASL 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564 LYNVNGLKAQPWWTPKETGYTELVKSLERNWKLIRDEGLAVMD----KAKGLFLPEDENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.7%; Score 189.5; DB 4; Length 312;
Best Local Similarity 27.8%; Pred. No. 2.5e-07;
Matches 52; Conservative 34; Mismatches 88; Indels 13; Gaps
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 9410 Key West Avenue CITY: Rockville STATE: Marvi---
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APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                Sequence 8015, Application US/09328352 Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 218, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Choi et. al.
TITLE OF INVENTION: Stree
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASCII Text
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                                                                                                                            965 P--PGD 968
                                                                                    412 PDVPAD 417
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                                                                                                                                                                                                                US-09-328-352-8015
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                                                                                                                         62 KEDSABPA-PVEEVGGEVESKPEEKVAVKPESQPSDKPAEESKVEQAGBPV---APRED 116
                                                                                                                                                                                                                                                                                                                                                                                              283
                                                                                                                                                                                                                                                                                                                                                                                                                                               EVPPETNR------KTD----DPEQKAKVKKKKPKLLNKFDKTIKAELDAABK 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 EVNSETNKLKTAIDALNVDKTELNNTIADAKTKVKEHYSDRSWONLOTEVTKAEKVAANT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 407 IKSITAELKKGEEVINTVVLTDDKVTT-ETISAAFKNLEYYKEYTLSTTMIYDRGNGEET 465
                                                                             111 ERSTSEPAVPPEE--AEPHTEPEEQVPVEAEPQNIEDEAKEGIOSLIHEMVHAEHVEGED 168
                                                                                                                                                                                                                                                                                                                117 EKAPVEPEKQPEAPEEE--KAVEETPKQEESTPDTKAEETVEP--KEETVNQSIEQPKVE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----EQQ 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 EDKIKGIGTKEPVDKSELNNQİDKASSVSPTDYSTASYNALGPVLETAKGVYASEPVKQP 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----KELVRKYPQSPRARYGKAQ 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 DAKQSEVNEAVEKLTATIEKLVELSEKPILTLTSTDKKILEREAVAKYTLE---NQNKTK 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 CEDDLAEKRRSNEVLRGAIETYQEVASLPDVPADLLKLSLKRRSDRQQFLGHMRGSLLTL 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 QRL----VQLFPNDTSLKN----DLGVGYLLIGDNDNAKKVYEEVLSVTPNDGFAKVHYG 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Choi et. al. TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                   169 IQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQ-DME
                                                                                                                                                                                                                                                                                                                                                                                              228 EMMSEQENPDSSEPVVEDE----RLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPP
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466 ETLENQNIQLDLKKVELKNIKRTDL-IKY-----ENGKETNESLITTIPDD---KSNYY 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 EVNSETNKLKTAIDALMVDKTELMNTIADAKTKVKEHYSDRSWQNLQTEVTKAEKVAANT 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 EMMSEQENPDSSEPVVEDE----RLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 TPAVEKOTEPTEEPKVEQAGEPVAPREDEQAPTAPVEPEKQPEVPEEEKAV---EETPKP 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.4%; Score 177.5; DB 4; Length 565; 22.5%; Pred. No. 5.5e-06; Live 71; Mismatches 199; Indels 123.
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
CORPUTER: HP Vectra 486/33
COPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-0ct-1997
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION: CURNOWN>
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: MICHORARY ANKS
RECERERATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 ED-----NPVEDSQV---IVEEVSIFPVE-----
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TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 218:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 516 LKITSNNOKTTLLAVKNIEETTVNGTP 542
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                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 218:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 565 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 22.5
Matches 114; Conservative
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Search completed: May 5, 2004, 11:05:05 Job time : 25 secs us-09-903-216-2.rapb

Page

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model

5, 2004, 11:03:59 ; Search time 48 Seconds (without alignments) 4377.285 Million cell updates/sec May Run on:

US-09-903-216-2 4022 1 MAQRKNAKSSGNSSSSGSGS.....IVDVWHPELTPQQRRSLPAI 758 Title: Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

1138120 segs, 277189581 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1806, Ap	Sequence 1806, Ap	Sequence 1806, Ap	Sequence 1806, Ap	Sequence 1806, Ap	Sequence 1806, Ap	Sequence 8153, Ap	Sequence 15, Appl
SUMMARIES		D	US-09-903-248-2	US-09-859-604-2	US-09-903-063-2	US-09-903-216-2	US-09-903-199-2	US-09-903-023-2	US-09-436-184-2	US-09-736-457-1806	US-09-902-941-1806	US-09-849-626-1806	US-10-283-017-1806	US-10-017-754-1806	US-10-113-872-1806	US-10-156-761-8153	US-10-168-274-15
		DB	0	9	0	σ	σ	σv	10	Φ	σ	σ	12	14	14	14	14
		Match Length DB	758	758	758	758	758	758	758	255	255	255	255	255	255	250	369
	ouerv	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	32.8	32.8	32.8	32.8	32.8	32.8	6.9	6.8
		Score	4022	4022	4022	4022	4022	4022	4022	1320	1320	1320	1320	1320	1320	275	274.5
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US-09-820-843A-16 US-10-282-122A-63593 US-10-101-487-58 US-09-765-272-218 US-10-101-487-58 US-10-101-487-58 US-10-102-81-15 US-10-128-714-310-5 US-10-282-122A-46112 US-10-282-122A-6078 US-10-282-122A-6025 US-10-282-122A-6025 US-10-282-122A-6025 US-10-282-122A-6025 US-10-282-122A-78811 US-10-101-487-53 US-10-282-122A-78811 US-10-101-487-53 US-10-101-487-53
1616 1616 1616 1616 1616 1616 1616 161
189.5 189.5 189.5 17.5 17.5 17.7 17.5 17.5 17.5 168.5
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQ 180
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                                                                              APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
APPLICANT: de la Monte, Suzanne M.
APPLICANT: Ince, Wedim V.
APPLICANT: Ince, Wedim V.
APPLICANT: Carlson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS FILE REFRENCE: 21466-032 DIVS
CURRENT APPLICATION NUMBER: US/09/903,248
PRIOR APPLICATION NUMBER: US/09/903,248
NUMBER OF SEQ ID AND: 199436,184
NUMBER OF SEQ ID NOS: 9
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100.0%; Pred. No. 1.5e-282;
ative 0; Mismatches 0;
              ; Sequence 2, Application US/09903248; Patent No. US20020102263A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 758
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Best Local Simi:
Matches 758; (
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US-09-903-248-2
US-09-903-248-2
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                                                                                                                                                                      301 PPVEBOOEVPPETNRKTDDPBOKAKVKKKPKLLNKFDKTIKAELDAABKLRKKGKIEEA 360
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                   181 QEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSE 240
                                                                                                                                   301 FPVEEQQEVPPETNRKTDDPEQKAKVKKKKPKLLNKFDKTIKAELDAAEKLRKRGKIEEA 360
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APPLICANT: Wands, Jack R.

APPLICANT: Wands, Alan H.

APPLICANT: Gel A Monte, Suzanne M.

APPLICANT: Gel AMONTE, Alan H.

APPLICANT: Ghanbari, Hossein A.

TITLE OF INVENTION: DIGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS

TITLE REPERENCE: 21486-032 CIP

CURRENT APPLICATION NUMBER: US/09/859,604

CURRENT FILING DATE: 2001-05-17

PRIOR FILING DATE: 1999-11-08

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 758
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100.0%; Pred. No. 1.5e-282;
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APPLICANT: Wands, Jack R.
APPLICANT: de la Monte, Suzanne M.
APPLICANT: Carison, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REFERENCE: 21466-032 DIV3
CURRENT APPLICATION NUMBER: US/09/903,063
CURRENT APPLICATION NUMBER: 09/436,184
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.1
LENGTH: 758
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ORGANISM: Homo sapiens
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100.0%; Score 4022; DB 9; Length 758;

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APPLICANT: Ince, Nedim
APPLICANT: Carlson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
CURRENT APPLICATION NUMBER: US/09/903,216
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/436,184
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
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              Indels
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Pred. No. 1.5e-282;
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                 758; Conservative
   Best Local Similarity
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Patent No. US20020122802A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
APPLICANT: Ince, Nedim
APPLICANT: Carlson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
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                                                                            Length 758;
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; Pred. No. 1.5e-282;
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Best Local Similarity 100.0
Matches 758; Conservative
SEQ ID NO 2
LENGTH: 758
TYPE: PRT
ORGANISM: Homo sapiens
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100.0%; Pred. No. 1.5e-282;
ive 0; Mismatches 0;
         CURRENT APPLICATION NUMBER: US/09/903,199
CURRENT FILING DATE: 2001-07-11
PRIOR PILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 758
FILE REFERENCE: 21486-032 DIV4
                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 758; Conservative
                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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RESULT 6 US-09-903-023-2 Sequence 2, Application US/09903023

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100.0%; Pred. No. 1.5e-282;
iive 0; Mismatches 0;
                                                                                                                                                       OF.
                GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
APPLICANT: de la Monte, Suzanne M.
APPLICANT: Carlson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: 21486-032 DIVI
CURRENT APPLICATION NUMBER: US/09/903,023
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 09/436,184
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 100.'
Matches 758; Conservative
Patent No. US20020146421A1
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 210121.49615
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
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                                                                                                                                                                              ; Sequence 1806, Application US/09736457; Patent No. US20020168637A1
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Watanabe, Yoshihiro
Johnson, Jeffrey C.
Retter, Marc W.
Marnerakis, Margarita
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Bangur, Chaitanya S.
Lodes, Michael A.
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98.8%;
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                                                                                                                                                                                                                                                                                                                     Carter, Darrick
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Mannion, Jane
                                                                                                                                                                                                                                                                                     Fanger, Gary
Vedvick, Tom
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                                                                                                                                                                                                                      INFORMATION:
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US-09-902-941-1806
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US-09-736-457-1806
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APPLICANT: de la Monte, Suzanne M.
APPLICANT: de la Monte, Suzanne M.
APPLICANT: Ince, Nedim
APPLICANT: Carlson, Rolif I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REPRENCE: R.I. Hosp. - Malignant Neoplassus
CURRENT APPLICATION NUMBER: US/09/436,184
NUMBER OF SEQ ID NOS: 7
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                 758
0; Mismatches
                                                                                               ; Sequence 2, Application US/09436184; Publication No. US20030031670A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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758; Conser
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LENGTH: 758
                                                                                       JS-09-436-184-2
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Matches 75
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661 RRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETRTWEEGKVLIFD 720
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                                                                                                                Score 1320; DB 9;
Pred. No. 1.9e-87;
1; Mismatches 2;
                                                                                           721 DSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI
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us-09-903-216-2.rapb

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61 VPPEBABPHTEPEEQVPVBABPQNIBDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE 120
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APPLICANT: Wang, Aljun
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia
APPLICANT: McNeill, Patricia
APPLICANT: McNeill, Patricia
APPLICANT: McNeill, Patricia
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APPLICANT: McNeill, Patricia
APPLICANT: McNeill, Patricia
TITLE OF INVENTION: DIAGNOSIIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSII OF LUNG CANCER
TILE APPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
SECTION OF 1806
LENGTH: 255
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Pred. No. 1.9e-87;
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APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Pedvick, Thomas S.
APPLICANT: Bedvick, Thomas S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C17
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FASTSEQ for Windows Version 4.0
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Publication No. US20020197669A1
PAPPLICANT: Bangur, Chaitanya
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US-09-849-626-1806
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ORGANISM: Homo sapiens
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LENGTH: 255
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179 PQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS
                                                                              61 VPPEBAEPHTEPEROVEVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 210121.478620
CURRENT APPLICATION NUMBER: US/10/283,017
CURRENT APPLICATION NUMBER: US/10/283,017
NUMBER OF SEQ ID NOS: 2157
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1806
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1806, Application US/10283017 Publication No. US20030211510A1 GENERAL INFORMATION:
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Vedvick, Thomas S.
Bangur, Chaitanya S.
McNabb, Andria
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Watanabe, Yoshihiro
Kalos, Michael D.
Sleath, Paul R.
Johnson, Jeffrey C.
Retter, Marc W.
Durham, Margarita
Carter, Darrick
Fanger, Gary R.
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US-10-283-017-1806
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Best Local Similarity
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US-10-283-017-1806
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LENGTH: 250
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APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Darrick
APPLICANT: Panger, Thomas S.
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APPLICANT: Wedvick, Thomas S.
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APPLICANT: Kalos, Michael D.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: APPLICALION: UNDIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.478C19
CURRENT APPLICATION NUMBER: US/10/113,872
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                                                                                                                                                                              ; Sequence 1806, Application US/10017754; Publication No. US20030054363A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              APPLICANT: Henderson, Robert A. APPLICANT: Wang, Tongtong
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98.8%;
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              241 SIFPVEEQQEVPPDT 255
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US-10-017-754-1806
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Best Local 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        569 GLKAOPWWTPKETGYTEL---VKSLERNWKLIRDEGLAVMDKAKGLFLPEDENLREKGDW
                                                                                                                                                                                                                                                                        59 MVIALLGVWTSVAVVWPDLVDYBEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
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                                                                                                                                                                                                                                                                                                                                                                     119 VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE
                                                                                                                                                                                                                                                                                                                                                                                               179 POQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS
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                                                                                                                                                                                Length 255;
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                                                                                                                                                                                Score 1320; DB 14;
Pred. No. 1.9e-87;
1; Mismatches 2;
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1 Similarity 33.3%; Pred. No. 9.2e-12;
65; Conservative 31; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YASHYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
NUMBER OF SEQ ID NOS: 2011
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1806
LENGTH: 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8153, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Streptomyces avermitilis US-10-156-761-8153
                                                                                                                                                                                    32.8%;
98.8%;
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UIN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                  Conservative
                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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526 RFYFHLGDAMORVGNKEAYKWYELG--HK----RGHF----ASVWORSLYNVNGLKAQPW 575
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684 NCRLRMHLGLVIPKEGCKIRCANETRIWEEGKVLIFDDSFEHEVWQDASSFRLIFIVDVW 743
                                           Query Match
6.8%; Score 274.5; DB 14; Length 369;
Best Local Similarity 30.1%; Pred. No. 1.7e-11;
Matches 75; Conservative 44; Mismatches 105; Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
Name/KEX: misc_feature
CTHEN INFORMATION: Incyte ID No. US20030124106A1 2754425CD1
US-10-168-274-15
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Sequence 15, Application US/10168274

Sequence 15, Application US/10168274

Sequence 15, Application US/10168274

Sequence 15, Application No. US20030124106A1

GENERAL INCYTE GENOMICS, INC.

APPLICANT: INCYTE GENOMICS, INC.

APPLICANT: APL. Preeti

APPLICANT: AAPLICANT: AAIGA, V. Tom

APPLICANT: AALWAN, Jennifer

APPLICANT: AAZMZAI, Yalda

APPLICANT: AZZMZAI, Yalda

APPLICANT: BAUGHN, MARIBER: US/10/168, 274

CURRENT APPLICATION NUMBER: 60/172, 367

PRIOR FILING DATE: 1999-12-16

NUMBER: OF SEQ ID NOS: 54

SEQ ID NO 15

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                                                                                                                                                                          744 HPELTPQQRRSLPAI 758
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ORGANISM: Homo sapiens
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